

TGAATAAACC GAATGTGGCT AAAGTCGTTA ACGCAAATA TGACGTCATC TATAACGGAC 120
 ATACTTTTGC AACATCTTTA CCAGCGnAAT TTGTAGTAAA AGATGTGCAA CCAGCGAnAC 180
 5 CAACTGTGAC TGAAACAGCG GCAGGAGCGA TTACAATTGC ACCTGGAGCA AACCAAAC 238

(2) INFORMATION FOR SEQ ID NO: 4533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4533:

GGTCATTAAT AAAATATCTA AAGCCATTAC TGCATAAAAA TCTCATCAAG CCAATACCTA 60
 20 CATTGTACTA CTGGnCACTT TAGACAGGnC AAGGGTGTAG CTACCGATAA TTCAGGAGCA 120
 TTAACGCAAC CGACATTTGA CTGTATTAAA TGATAGAGGT TCTGGAAAAC GCCCCAGGTG 180
 GTGGAGTTCA AGAAATAATT CACAGGGCTG ACGGAACATT CCTGCACCCC AAGGACGAGA 240
 25 TGTGGTTGTT CCACTAGGAG TTGGAA 266

(2) INFORMATION FOR SEQ ID NO: 4534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4534:

TACTCAGAGG ATACCCCGAC GTAATGCATT CAATTCAATT TTAAACGTA TTATTTCAATT 60
 40 GAGCAGAAAG AAAATTATGG CACCAAACCTT TAATATTTTT TTCAATGTCA TTCTTTTGAn 120
 GGGAGTGGGA CAGAAATGAT ATTTTCGCAA AATTTATTTTC GTCGTCCAC CCCAACTTGG 180
 CATTGTCTGT AGAAATTGGG AATCCAATTT CTCTTTGTnG GGGCCCATCC CCAACTTGCA 240
 45 CATTATTGTA AGCTGACTTT TCGT 264

(2) INFORMATION FOR SEQ ID NO: 4535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4535:

GCGAATGGAT AACAGTTGAT ATTCCTGTAC CACCTGATAA ATCGTTTTAA TCGATGGGGG 60
 5 GACGCATAGG nATAGGCGAC TGCCGATTGG ATTGCACTCT AAGCAGTAAG GCTGAGTATT 120
 AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA 180
 GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AAATAGGTGC CCCGTACnGC 240
 10 AAACCGACAC 250

(2) INFORMATION FOR SEQ ID NO: 4536:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4536:

AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 60
 25 AATTCTCCGA TTAAAACTG CCTGGCAACG TTCTACTCTA GCGGAAnTAA TTCGAACTAC 120
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180
 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAnATAGT AAGTA 235

(2) INFORMATION FOR SEQ ID NO: 4537:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4537:

TGCATCTTCA CAGGTACTAT GATTTACCCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 60
 TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT 120
 45 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAG CTAACCACTC 180
 CTCTTAACCT TCCAGCACCG GGCAGGCGTC AGCCCTATAC ATCACCTTAC GGTT 234

(2) INFORMATION FOR SEQ ID NO: 4538:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4538:

5 ACCCTCTGCT TGTnAGGCAG ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAACTGC 60
 CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGACTACC ATCGACGCTA AGGAGCTTAA 120
 CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CTCCTTGCT ATAGTCACCA GACATATGAA 180
 10 TGTAATTTAT ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACCATT 240
 TA 242

(2) INFORMATION FOR SEQ ID NO: 4539:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4539:

25 TCATTAACAC CATCACCATA AATAAAACCT TCCATATCTG TTCCTGTGCC AATAAAGCCA 60
 TATTGCGTTT GGnCTGTCGT GCCAGTGCAA GATTTC AAC GATAATTTCT AGGCGTCACT 120
 GCTGGCGAAC CATCTAATGG ATAATCATAA TCCATCGTGC GTCCAAGAAG TACTTGnTTT 180
 30 ATTTAAAGTT TGTATTGTGG AATCCTGTGC ACATGTTCTC ACTCCTCTGT ACCT 234

(2) INFORMATION FOR SEQ ID NO: 4540:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4540:

ACACAAAGAA AAATGGCTTG GCGAAGTGAA AACnGTTGAA TCTGACGAAA CGAGAAAAGA 60
 45 GCGCAACGAG TTTAGTAGAG CTAAATGAGT AAGCGAGACC GAAGAGAGGA AAGAAGCnAG 120
 CGATTGTCAC AAGTCAAGAA AGGTTCTTAG CGAGGATGGT AGCTAACTTA CGTTCCGCTA 180
 GAGTAGAACG TTGCTAGACA AGAAATGAAT GCGATGAGCC GCATTGAGTG TGAAATTGAT 240
 50 AT 242

(2) INFORMATION FOR SEQ ID NO: 4541:

55

(A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4541:

10 GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATATA GTCAAACGCT CACATACGGC 60
 TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120
 ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT 180
 15 GnAGTGTTCCT TTCGAACATA GGCGATTATn TCTTATGAAT TCAAGCTTAT TTAAAACTCT 240

(2) INFORMATION FOR SEQ ID NO: 4542:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4542:

AAGCTAGCAA TGATGTCAAG CAATGGCAAC ATGTGCTCAn TTAGCTAATA TGCAAGCACA 60
 30 TGGTGAATAT GACGAGGTTG CAACTTCAAC GGCGAGGnTG ATGAATGCCT TACGTTTGGC 120
 TGAGACAGTA GCTATGGGCC GCGGTATTAC AGGTGGTAAT GGCATACTGA GCTGACGATT 180
 ATGATATTGT CACGTTTTCT TCTCTGTATG CAGAAGCGAT TTACACGTAC GAGGTACACA 240
 35 TG 242

(2) INFORMATION FOR SEQ ID NO: 4543:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4543:

TGGTGAGCCA TAGAGGATTC GAACCTCTGA CCCTCTGATT AAAAGTCAGA TGCTCTACCA 60
 50 ACTGAGCTAA TGGCTCTTCC ATGGTGCCGG CCAGAGGACT TGAACCCCCA ACCTACTGAT 120
 TACAAGTCAG TTGCTCTACC AATTGAGCTA GGCCGGCAAT ATGTAAGATT AAATGGTGGA 180
 55 GAnTGACGGG TTCGAACCGC CGACCCTCTG CTTGTAAGGC AGATGCTCTn CCAGCTGAG 239

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4544:

ATAGAGGATT CGAACCTCTG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC AACTGAGCTA 60
 ATGGCTCTTC CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA 120
 GTTGCTCTAC CAATTGAGCT AGGCCGGCAA TATGTAAGAA TAAATGGTGG AGAATGACGG 180
 GTTCGAACCG nCGACCCTCT GCTTGTAAGG CAGATGCTCT nCCAGCTGAG CTAAATTCT 239

(2) INFORMATION FOR SEQ ID NO: 4545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4545:

AATTCATGCT TTCAAAAGAC GATATACTAC GACACTCCTA CGAACTTGTC CAAGGATTAC 60
 GAAAAGACCT AAGGTTATGT AATTGGCCTA AATTTATTAA TCGTTTAAAT TCAGTTAGTA 120
 AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAATA TTATAGAAAA CATCAAAGGA 180
 TGTTAAGAAA TACnATTTAT TACCCAGCAT TTAATAATGG TGCTATAGAA GGA 233

(2) INFORMATION FOR SEQ ID NO: 4546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4546:

ACTTTGTTGT CTTCCATCAA CTTGAGACTT CATAACGTTT TGCATCTTCG CCACCTTCAC 60
 CACTATTACT CTTCCACCT AATTGGTTCA TGGCTTGTC TAnTTTTTCA TGTGCTTCCG 120
 CTGAAATCGA TCCATAACTC ATCGCCCCTG TATTAAAGCG TTTGACAATG TCACCTACCG 180
 GTTCAACTTG GnCGATGTCA ATCGGTGTAC ATGCTTTAAA TTCAAGTAAA TGTCTAATGT 240

(2) INFORMATION FOR SEQ ID NO: 4547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4547:

GAGGAAATTA CTGAAAACAA TCATCATATT TCTCATTCTG GTTTAGGAAC TGAAAATGGT 60
 CACGGTAATT ATGGCGTGAT TGAAGAAATC GAAGAAAATA GCCACGTGGA TATTAAGAGT 120
 GAATTAGGTT ACGAAGGTGG CCAAATAGC GGTAATCCAG TGCATTTGAG GAAGACACAG 180
 AAGAAGTTTA AACCGAAATA TGAACCAAG GTGGGCATTA TCGTTGGTTA TCGATTTTCG 240
 ATAGTGTACC TCAAATTTCA TGGGTCCAAA TTAATGGTTA ACCCATCCAT TCGAnGnAGG 300

(2) INFORMATION FOR SEQ ID NO: 4548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4548:

TTGCTATAGT CACCAGACAT ATGAATGTAA ATTATACATT CAAAACTAGA TAGTAAGTCA 60
 AAGTGATTTT GCTTCGCAAA CATTTATTTT GATTAAGTCT TCGATCGATT AGTATTCGTC 120
 AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGGA 180
 TCTTGATAAA CCGnAAGTTG GGGAAATCTC ATCTTTACGG GGGGGCTTCA TGCTTAGGAT 240
 GGCTTTnCAG CACTTTATGC CCGGTnCCAC ACATTAGGCT TACCCAGCCT ATGCCCCGTTT 300
 GGCACG 306

(2) INFORMATION FOR SEQ ID NO: 4549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4549:

CTTCTACTTT TGTACCATCA ATAAGATTTT GCTTTAAACA TTGACTATGA AACTGGATAA 120
 ATAAAGATTG AATTAACGCA TCAGTATTAG GATTCACTCT AATACGATTA ATAGTTTTAT 180
 5 AAGAAGGTGn TTGATTTTGA GCTAACCACA TCATTGGAAT ACTGTCATGn AG 232

(2) INFORMATION FOR SEQ ID NO: 4550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4550:

CTGGGTTTCAG AACGTCGTAT GnAGTTCGGA TCCCTATCCG TCGTGGGCGT AGGAAATTTG 60
 20 AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG TACCAGTTGT 120
 CGTGCCAAng CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AACATTCTTA 180
 AGCATGAAGC CCCCCTCAAG ATGAGATTTT CCAACTTCGG TTATAAGATC CCTCAAAGAT 240
 25 GATGAAGTTA ATAAGTTC 258

(2) INFORMATION FOR SEQ ID NO: 4551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4551:

TTACAGGCAT GCGAGTTGGG GTGAGGGCCC ACACAGAAGC TGACGAAAAG TCATGACAAT 60
 40 AATGTGCAAG TTGGGGATGG GCCCACAAAG AGAAATTGGA TTCCCAATTT TACAGACAAT 120
 GCAAGTTGGG TGGGACGACG AAATAAATTT GCGAAAATAT CATTTCTGTh CCCTCCCTCA 180
 AAAGATGACA TTGAAAAAAT ATTAAAGTTG GTGCCATATT TTCTTCTGCT CATGAATATA 240
 45 CGTTAAAATT GATTGATCAT CGCGAATTGA TATTATTCTC ATTATAAAAA TACTTATTAC 300
 ACTTACCGTA TGATAGTTTG nTATATACTC TGATAAAGTC AAACCTAATA GCGTTTCTAG 360
 CTGTGnGTGT TTCATAATTA TATACATTAT CAGGCTTTAA 400

(2) INFORMATION FOR SEQ ID NO: 4552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4552:

	ATAGGAAACT GCCAATTGGA CGGTTGCCGC ATTCAAACCC AGCACGATTA CGGCGAATTG	60
10	CACGTGAAnC ATTTCTACAG CTTGATCTTG ACCTATGATT TTA CTCTTA AACGATTAGA	120
	AATATTTTTT AAACGTTCAA TATCGTTATC ATCCATTTGG AGAAACTGGG AATACCATTG	180
	AATCGTTGnA ATAGTATCTG GAAATATCAT GGAAGTGTAG CAACAGCAGT GTGTTGCACC	240
15	ATTnACTGAT TTTGCTAATT TATCTTGGTG AATGGATTTG GATTTGCATT TTGGAATGTG	300
	CGTGCAGCTT TT	312

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(2) INFORMATION FOR SEQ ID NO: 4553:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4553:

30	AGCAGCGATC AAAAATAATC CGCAATACGC TGGCAAATA CCAATACCAA ACCATAGAAC	60
	AACAAATGGT GCCCATGCTA TCGGAGATAT CGGCCTAATC AATTGAAATA GCGGTTTCGAT	120
	AGCGTTGTAT AGCCAACGAT TCCTTCCAAG CAAGAAGCCC AATGGAATAG CAACCAACAA	180
35	TGCGACAACA AAGnCCGCTA CAAATCTCCA TGAAGTAATT GCTAAATGTG GnGAATTTCT	240
	CCAGTAACAA TGGA	254

40

(2) INFORMATION FOR SEQ ID NO: 4554:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4554:

50	GGTCTGAATC GCTATCTGAG TCTGAATCGC TATCTGAGTC TGAATCACTG TCTGAGTCn	60
	AGTCACTGTC TGAATCTGAC TCACTATCTG ATTCTGAGTC GCTATCTGAT TCTGAGTCGC	120
	TGTCTGGAAT CTGAATCACT GTCTGGAATC CGAATCGCTA TCTGGATCTG AGTCGCTATC	180

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CTGGGGCTTG G

251

(2) INFORMATION FOR SEQ ID NO: 4555:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4555:

TACACAAAGA GATAAATTAC TTATGCAAAG GCGGAGGAAT CACATGTCTA TTACTGAAAA 60
ACAACGTCAG CAACAAGCTG AATTACATAA AAAATTATGG TCGATTGCGA ATGATTTAAG 120
AGGGAACATG GATGCGAGTG AATTCCGTAA TTACATTTTA GGCTTGATTT CTATCGCTTC 180
CTATCTGAAA AAGCCCnACC AGAATATGCA GTGCCCTGTC AAGnGAAGAC ATCACGTTCC 240
AGAAGCATGG C 251

(2) INFORMATION FOR SEQ ID NO: 4556:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 243 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4556:

AGCTACCCCG GGGATAACAG GCTTATCTCC CCAAGAnTT CGCATCGACG GGGAGGTTTG 60
GCACCTCGAT GTCGGCTCAT CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT 120
TCGCCCATT AAGCGGTACG GAGGCTGGGT TCCGAACGTC GTGAGnCCGT TCGGTCCCTA 180
TCCGTCGTGG GCGTAGGAAT TTGAGAGGAG CTGTCCTTAG TACGAGAGGA CCGGGTGGAC 240
ATA 243

(2) INFORMATION FOR SEQ ID NO: 4557:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4557:

TCATTATTTT AAATGCTCAT TTACATAAGT AAACCTCTGCT TTAAAATAAT TTAACTCATT 120
 GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTAAACGCG TTATTAATCT TGTGAGTGTT 180
 5 CTTTCGAACA CTAGnCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTG 235

(2) INFORMATION FOR SEQ ID NO: 4558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4558:

CCGTTAAGCA CTAAATCCGC TTAATAACGG CTTTCTATCG CGCGCAACAT CTCGTTTGAC 60
 20 TGCTTTTTTCT TTCAAAGCTT GACGTTATCA TATTTTTTCT TACCTCGTGC ACACCAAGTA 120
 ATACTTTACA ATGTCCATGC TTCAAATAAA GCTTTAACGG ACAATCGAAT AACCAAnCTC 180
 ACGTGTTTGA TCACCCAATT TAATGATTTT ACGCTTGTGC AATAATnATT TTCGAGACGA 240
 25 GAGGATCGGA TTAAACGAT CCCCTCCTCG TATGG 275

(2) INFORMATION FOR SEQ ID NO: 4559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4559:

TTATATGGAT GTATCGCCGA AGCAAGTTGT TTCAGCAGCG ACAnATGTAT TCCGATGACT 60
 40 CAAACCGTGC ATTGATGGGT GCGAACATGC AACGTCAAGC AGTGCCTTTG GATGAATCCA 120
 GAAGCACCAT TTGTTGGTAC AGGTATGGAA CACGTTGCAG CACGTGTATT CTGnGTGCGG 180
 CTATTACAGC TAAAGCACAG AGGTCGTGTT GAACATGTTG GAATCTAATG AAAT 234

(2) INFORMATION FOR SEQ ID NO: 4560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60
 TTCTACTCTA GCGGAAnTAA nTGGCTACCA TCGTCGCTAA AGACCTTTCT TGACTTGTGA 120
 5 CAATCGCTTG CTTCTTTCCT CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTACTAACT 180
 CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA AG 232

(2) INFORMATION FOR SEQ ID NO: 4561:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4561:

20 TCAAAGGACG CATACCATTA CGGGTCTGCT ACTTGTAAGC ACACGGTTTC AGGTTCTATT 60
 TCACTCCCCT TCCGGGGTGC TTTTnACCTT TCCCTCACGG TACTGGTTCA CTATCGGTCA 120
 CTAGAGAGTA TTTAGCCTTA GGAGATGGTC CTCCCAGATT CCGACGGAAT TTCACGTGCT 180
 25 CCGTCGTACT CAGGATCCAn TCAAGAGAGA CAACATTTTC GACTACAGGA TTATTACCTT 240
 CTTTGATTCA TCTTGTC 257

(2) INFORMATION FOR SEQ ID NO: 4562:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4562:

40 TACCTAATAA GTTGTGAATT TGAACAGCGG CTGCTTTACA nTGGAAGTGC TGATTCAGTT 60
 GCCACAATTA CCATACCAAT TTTCTTTTGT TCTTCGTCTG TnATAATGTC CTTAGCAGCG 120
 TTAGCTCCGA TTGAAACGAT GTCTTGGTTT ACAGGACTAA CAGCCATTTTC AGTTTGACCA 180
 45 ATTCCAATTA AAAATTTGTT TGGGTCTACT TGGCGTGGCT TCCTGCTGAA TTTAGCCATG 240

(2) INFORMATION FOR SEQ ID NO: 4563:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4563:

CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 60
 5 TAGTGCCAAG GCATCCACCG TCGGCCCTTA ATAACTTAAT CTATGTTTCC ACCATTTTAA 120
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTATTTT AnATGCTCAT TTACATAAGT 180
 10 nGACTCTGCT TTAAAATAAT TTAATCATT GTCTGCTAAA CGTTT 225

(2) INFORMATION FOR SEQ ID NO: 4564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4564:

TGTTAATTGG nGAATTTGGA TACTGGTTAT ATTCAGCTGC ACCGCAAGCA ACTTCTATTG 60
 ATGGCCTAAC TGCCTTTTTA CCTCAAGCAA TGGGTATGGT AATTGTTGCA GTCATTTATG 120
 25 GCTTTATGAA TATGAAAGCA GAGGAATCCC ATTCCCGTAA TAAAATTACG GTGGTTACAA 180
 AATTATTCA GGTTCCTTC TTTTGCATTT GGGTGCTTTA ACCATATCTT nTT 233

(2) INFORMATION FOR SEQ ID NO: 4565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4565:

AGCTCAGATA GCGCTCAGAC TCAGACAGCG ACTCAGATTC AGATAGCGAT TCAGACTCAG 60
 ACAGCGACTC AGACTCAGAC AGCGACTCAG ACTCAGATAG CGACTCAGAT TCAGATAGCG 120
 ATTCAGACTC AGACAGCGAC TCAGATTCAG ATnGCGATTC GGAnTCAGAC AGCGATTCAG 180
 45 ATTCAGACAG CGACTCAGAC TCGGATAGCG ATTCAGATTC AGATA 225

(2) INFORMATION FOR SEQ ID NO: 4566:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4566:

CCAACTGGAG CTAATGGCTC TTCCATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 60
 5 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAATGG 120
 TGGAGAnTGA CGGGTTTCGAA CCGCCGAnCC TCTGCTTGTG AAGGCAGATG CTCTCCCAGC 180
 10 TGAGCTAATT CTCCGATTTA AAActGGCCT GGGCAACGTT CTAActTAGC GGGAAct 237

(2) INFORMATION FOR SEQ ID NO: 4567:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4567:

GTTGGAGATA GTGTAATAAT GCCAATGAGC CACTCTGAAG TTACAGCGGA TGGGTGTTTT 60
 GCCAAAATTC CATGGTGGTA CGAAAAAGAA AAAATGGATG GAAACAAGTT ACTGAAAATC 120
 25 TTGGTAAAAA AGCAGGGGAC TTCGGTTCTA AAGCTAAAAC ACAGCTCATA ATATCAAAAA 180
 GGTGCAGAGG AAATGGTTGA nnGGCAGCGG ATAAATCAAG ATGGTGCACT TGGTTAGCGT 240
 30 TAAATCGCGA TGTGTGGGTT AnTACACATC CGGGAActAG TAATAAGTAT GTCAGTTTAA 300

(2) INFORMATION FOR SEQ ID NO: 4568:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4568:

ATCCCGTGGA GGTTCAAGTC CTCTCGGCCG CATCAAAATT CTTAATTTAA ATAAGCGGGT 60
 GTAGTTTAAT GGCAAAACCT CAGCCTTCCA AGCTGATGTT GTGGGTTCGA TTCCCATCAC 120
 45 CCGCTCCATA GATAATTTTA ATGAACATTG AAAActGAAT GACAATATGT CAACGTTAAT 180
 TCCAAAAACG TAACTATAAG TTACAAACAT TnATTTTAGT ATTTGATGGA GCCTnAATCC 240
 50 AAACATTCCA 250

(2) INFORMATION FOR SEQ ID NO: 4569:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4569:

GATCCCCTAG CTTTACGTTC AACTTTATAT GGGTATAACT CGAATATAAT TTGGCGCTCT 60
10 ATGTCATGGG ACAACGAGTA GACATTTAAT AACGGATCAG GTTCTGGTGA CGGTATCGAT 120
AAACCAGTTG TTCCTGAACA ACCTGGTGAG CCTGGTGAAA TTGAACCAAT TCCAGAGGnT 180
TCAGATTCTG ACCCAGGTTC AGATTCTGGG CAGCGnTTCT AATTCAGATA GCGGT 235

15

(2) INFORMATION FOR SEQ ID NO: 4570:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
20 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4570:

AATCTATTTT TTCTATTGTT AAATCGCTAT CTCCATCTTC TTTTATCTCT GGTATTATTT 60
TTTCTTCAAC TAAGTCACGA TATAATGTTT TTGAATTTTC GTTCAATTTT GATTTCGTGAT 120
30 TTTGAATACT TTTCTTCCAC ACAAATGTAT ACCTATTGGC ATTAGCnTCT ACTTTTGTAC 180
CAnCAATAAG ATTTTGCTTT AAACATTGAC TATGAAACTG GGA 223

(2) INFORMATION FOR SEQ ID NO: 4571:

35

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 267 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4571:

CATGATATTT TGAACCGCAT GGTAAAGTT GCAAAGACGG TCTTGCTGTC ACTTATAGAT 60
45 GGATCCGCGC TGCATTAGCT AGTTCGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG 120
CCGACCTTAG AGGGTGATCG GCCACACTGG nACTAAGACA CGGTCCAGAC TCCTACGGGA 180
50 GGCAGCAGTA GGGAAATTTTC CGCAATGGGC GAAAGCTGTA CGGCGCAACG TCGTGTGnAG 240
TGCTGCAGGT TCTTCGGATC GTAAAAT 267

(2) INFORMATION FOR SEQ ID NO: 4572:

55

(A) LENGTH: 221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4572:

10 AATnCAACTT TTACTIONACTA TCTAGTTTTG AATGTATAAA TTACATTCAT ATGTCTGGTG 60
 ACTATAGCAA GGnGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG 120
 TCGATGGTAG TCGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAT AATATTAATC 180
 15 CACAGTAGCT CAGTGGTAGA GCTATCGGCT GTTAACCGAT C 221

(2) INFORMATION FOR SEQ ID NO: 4573:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4573:

GCAGAAATGC CAGCCGCATT GAGTGAACAC AGAGTTACAG GGTATTCTGT AGCCGAACCA 60
 30 TTCGGTGCA n TGGGGGAAAA GTTAGGCAAA GGTAAGACTT TGAAACATGG TGATGACGTT 120
 ATACCTGATG CGTATTGCTG TGTGCTAGTA CnAGAGGGG AATTGCTTGA TCAACACAAG 180
 GATGTAGCGC AAGATTGTA CAAGGTTATA AAAAGTCTGG CTTTAAAATG 230

(2) INFORMATION FOR SEQ ID NO: 4574:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4574:

45 TCACATATCG ATAACATGAC ATAACATCATG CTGGGTTTCC CCATTCGGAA ATCTCTGGAT 60
 CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 120
 50 TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACCTAAT CnATGTTTCC ACCATTTTTTA 180
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTAnTTT AAATGGCTCA 230

(2) INFORMATION FOR SEQ ID NO: 4575:

(A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4575:

10 CTTACAATAG TGTGCAAGTT GGGGTGGAGC CCCGACACAG AGAAATTAGC TCCTCAATTT 60
 CTACAGACAA TGCAAGTTGG CGGGGCCCCA ACACAGAAGC TGGCGAAAAG TCAGCTTACA 120
 ATAGTGTGCA AGTTGGGGTG GGACGACGAA ATAAATTTTG CGAAAATATC ATTTCTGTCC 180
 15 CACTCCCAAA AAGACCGCAG TAGGATAATT CCATTTGGAA ATACCTTACT GCCnGTTTTT 240
 AAAGTAATAG CnAATATTTT GGAATTAnGT TTCCTAGTTA ACCATACCAA CTAATGGCCT 300
 CCTTAAATT 309

20

(2) INFORMATION FOR SEQ ID NO: 4576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4576:

30 TGATTCTAGG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGGTAAA 60
 ATCTATATTT TACTTACTTA TCTAGTTTTT AATGTACAAA TAATGGTGGG CCTAAGTGGA 120
 35 CTCGAACCAC CGACCTCACG CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCCC 180
 ATTTTTTTTGA ATGTTAAATA AACATCnAAA CTGGnATACC ATATGTCACG GTAATCCGCA 240

(2) INFORMATION FOR SEQ ID NO: 4577:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4577:

50 CTTCGTGTTA AAATTTGATG CACAATGGTC ATCATTTTTTA TCTTTCCAAT AAGTACTGTC 60
 TGGGTAAAAA TnTATTAAATT GGGTGGTTCG TGAAATGCAA TCTTTTTTAAC GACTTCAGGG 120
 TAATCTTTTA ACACATGCAT CGCAACGATT GAACCTnAAC TTGAACCTAA TATATAGACA 180

55

(2) INFORMATION FOR SEQ ID NO: 4578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4578:

TAGGCATACC AAAGTCGATA CCATAGTGAC GACCGCCATT AAAGTTAAGT CCACCTGTGT 60
 AACTCCCAAA CCTTTGCCAA ATTGGATGGT CAAATAGATA GCTTCCATCG CCTCCGCCAC 120
 CAAAATCTTC AAACCACGAT TTA CTTTGn C TACTAATTTT TTTTGTAGCA ATGAGTACGC 180
 GCCTTAGCAA TTTTAnGTAG CGTAGTCCGC TCCAAAATAA TATTAAACTG ACATACTTAT 240
 TACnAGTTCC CTGGATGTGT ACATAATCCA CACATCGCGA TTTATCGCTA ACAGAGCACA 300
 CTTGATTACG CGCGCTCAAC ATTC 324

(2) INFORMATION FOR SEQ ID NO: 4579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4579:

AATGTAAAAA CTGATTTCTA TTAATTATTT GATAGAAATC ACTTTTTTGT ATTTTATAAT 60
 GTACAGCTCG TTGCATTCAT ATAGCTTGAA GTCACGTTTA AAACCATATC TATCATTATG 120
 GTATGCATAT CGTTTAAAC CTATTCTTTT GTTAnTAGGA CATATAAATT CATCATTAAT 180
 TCGTCATATT TCCAATTTTG AGTGThAAAA ATGTCACTTT TAAACTTTC 229

(2) INFORMATION FOR SEQ ID NO: 4580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4580:

CGGGGACTCn AACCCGTGTT GACCGCCGTG GAAAGGGCGG TGTCTTAACC GCTTGnACCA 60

CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA 180
 CGTAAGTTTCG ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCCGC ATGGGAACA 239

(2) INFORMATION FOR SEQ ID NO: 4581:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4581:

CCGnACGAAT TTACACGTGT TCGTCGTAC TCAGGATCCA CTCAAGAGAG ACAACATTTT 60
 CGACTACAGG ATTATTACCT TCTTTGATTC ATCTTTCCAG ATGATTCGTC TAATGTCGTC 120
 CTTTGTAACCT CCGTATAGAG TGTCCTACAA CCCCAACAAG CAAGCTTGTT GTnTTGGGCT 180
 CTTCCCGTTT CGCTCGCCGC TACTAAGGGA ATCGAATTTT CTTTCTCTTC CTC 233

(2) INFORMATION FOR SEQ ID NO: 4582:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4582:

TTAGTAAAAA GTCTGTGAGT AAGGGTGTAT GGAAAGTGGT TAAATATTAT AGAAAACATC 60
 AAAGGATGTT AAGAAATACA ATTTATTACC CAGCATTAA TAATGGTGCT ATAGAAGGAA 120
 TTAATAATAA GATAAAATTA ATCAAGTGAA TTTCTTTTGG TTACAGAAAT TTCAnCanCT 180
 TTAAAGCACG TATAATGATG GATTTTCAGC TTGTACAA 218

(2) INFORMATION FOR SEQ ID NO: 4583:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4583:

TAATAAACAT GCCATACGTA ATAAGTGGCG TTGTATTAAA ATCATCTATA ATAGCCATAT 60

ATTTTGAAT CATTGTAA AATGGAATTA AAGTTCTAGT GATCTGTTGG GTTTTGGAAA 180
 TAGGTCATAG GGTnAAAACn TTTTGTAGAA TTTGTCGCTA TTTGTTAAAT TGTATCCCGG 240
 5 CTTGAAGTTG G 251

(2) INFORMATION FOR SEQ ID NO: 4584:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4584:

TTTAGGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTCTGTA GCTTCGCAGA 60
 20 nTAACCCACT CCTCTTAACC TTCCAGCACC GGGGCAGGCG TCACCCCTAT ACATCACCTT 120
 ACGGTTAGCA GAGACTGTGT TTTTGATAAA CAGTCGCTnG GCCTATTCAA TGGGGGCTCT 180
 25 TCTGGGGGTT AAACCTAAAG AGCAACCCTT CTCCCGAAGT TACGGGGTC 229

(2) INFORMATION FOR SEQ ID NO: 4585:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4585:

TTATAAAAAG ATTTAAACGC GTTATTAAATC TTGTGAGTGT TCTTTCGAAC ATAGCGATTA 60
 TTTCTTATGA ATTCAAGCTT ATTTAAAACT CTTTATTCAC TCGGTTTTGC TTGGTAAAT 120
 40 CTATATTTAC TTACTTATCT AGTTTTCAAT GTACAATTnC TTTTtagTCA AGCGCTCGCA 180
 TACTGCTnTA TTTTCAAAAA ATCAAATGCT CATTTACA 218

(2) INFORMATION FOR SEQ ID NO: 4586:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4586:

GGAATTCCAC TTTCCTCTTC TGCACTCAAG TTTTCCAGTT TCCAATGACC CTCCACGGTT 120
 GAnCCGGGGC TTTTCACATC AGACTTAAAA AACCGCCTAC GCGCGCTTGT ACGCCCAATA 180
 5 ATTCCGGATA ACGCTTGCCA CCTACGTATT TACCGCGGGC TGCTGGCACG TATThAGCCG 240
 T 241

(2) INFORMATION FOR SEQ ID NO: 4587:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4587:

20 CAGCCACCTG TTGCCACCAG CTACACTTGC ATTGTTTGCT ACGACACGCC CAAACAATGC 60
 TGAAGTGAAT AAGAAATCAA TCATTTGCTC TTCTGTAA TCAATGTGTTT TTTCTAATTT 120
 AAAAAGTGCA CCGGGAATGG TACCCGAGGA ACCAGCTGTT GGCGTTGCAC AAATAATACC 180
 25 CATCGCAGCA TTGACTTCAT TGTTCGAAGG CACChTTGAC TGCGGCAATC ATTCATATCC 240
 GACnAAGCAG ATG 253

(2) INFORMATION FOR SEQ ID NO: 4588:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4588:

40 ATGAACGGGT GGTAGCGAGT GGACGAAAAA CATCAATGAA AAGCTAGCTG TAGTTGCAAG 60
 AGAAACTGGC TTACGATGGC ATTGGATCAA CACATGCGGC ATTGAGAAAT CCACGCATGG 120
 CTGAGACGTT TACGATTGCG CGAAAAATGA ATCCTGAAGG CATTTTtagCA ATGTTGGTGC 180
 45 GGACGTACCA GTAGAAAAGG CTTTGGAAGC AGTTGAAT 218

(2) INFORMATION FOR SEQ ID NO: 4589:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4589:

5 GCCATGGCTC CACAGGTAGG ACTCGAACCT ACGACCGATC GGTTAACAGC .CGATAGCTCT 60
 ACCACTGAGC TACTGTGGAT TAATATTATG CCTGGCAACG TTCTACTCTA nCGGAACGTA 120
 AGTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT 180
 10 GACCTCCTTG CTATAGTCAC CAGACATATG nATGTA 216

(2) INFORMATION FOR SEQ ID NO: 4590:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4590:

20 AGATTTAAAT AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC 60
 ATCnATTCA TTTCTTGTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT 120
 25 CCTCGGCTAA GAACCTTTCT TGAATTGTGA CAATCGGCTT GCTTCTTTCC TCTCCTTCGG 180
 CTCTCGCTAC TCAATTTAGC TCTACTAAAC TCGGTTGCGG CTCTTTTCTn GTTT 234

(2) INFORMATION FOR SEQ ID NO: 4591:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4591:

40 AATTGACTGA CTTCGTTTTA CCGCGTGTTT AATATTGTTA TACATATATT CTAATTGCAC 60
 ATTTAAACTT CGTAAATGCC AATGTGnGTG GGACAGAAAT GATATTTTCG CAAAATTTAT 120
 45 TTCGTCGTCC CACCCCAACT TGnCACATTA TTGTAACCTG ACTTTCCGCC AGCTTCTATG 180
 TTGGGGCCCC GCCAACTTGC ACATTATTGT AAGCTG 216

(2) INFORMATION FOR SEQ ID NO: 4592:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4592:

ATTCCGGATA ACGCTTGCCA CCTACGTATT ACCGCGGCTG CTGGCACGTh TTAGCCGTGG 60
 5 CTTTCTGATT AGGTACCGTC AAGATGTGCA CAGTTACTTA CACATATGTT CTTCCCTAAT 120
 AACAGAGTTT TACGATCCGA AGACCTTCAT CACTCACGCG GCGnTGCTCC GTCAGGCTTT 180
 CGCCATTGCG GAAGATTCCC TACTGCTGCC TCCCCG 216

(2) INFORMATION FOR SEQ ID NO: 4593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4593:

TTGGACTAGA ACCAATGAAG GACGTTACTA ACGACGATAT GCTTAAAGGA GCTGTAAGTA 60
 AGCTTTGATC CAGAGATTTC CGAATGGGGA AACCCAGCAT GAGTTATGTC ATGTTATCGA 120
 25 TATGTGAATA CATAGCATAT CAGAnGGCAC ACCCGGAGAA CTGAAACATC TTAGTACCCn 180
 GTGGAAGAGA AAGAAAATTC GATTCCCTTA GTAGCGGCGA GCAGAACG 228

(2) INFORMATION FOR SEQ ID NO: 4594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4594:

CAATCGTTGA AGGAAATGTA CCAGCAGCAA TCAAAGACAA AGAAATTATT TCTGTAGACA 60
 TTTCATCATT AGAAGCTGGA ACGCAATATC GTGGTGCTTT TGAAGAAAAT ATTCAAAAAT 120
 TAATCGAAGG TGTAAATCT TCACAAAATG CCGTACTATT CTTTGATGAA ATCCATCAAA 180
 45 TTATCGGTTT AGGTGCCACA GnAAGTGGAT TCCAGGTTAG CCAAAGGGGT TAATCTGGAT 240
 TAATTTTTTT Th 252

(2) INFORMATION FOR SEQ ID NO: 4595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4595:

5 ACTCTCTAGT GACCGATAGT GAACCACTAC CGTGAGGAGA AGGTGAAAAG CACCCCGGAA 60
 GGAGnTGAAA TAGAACCTGA AACCGTGTGC TTACAAGTAG TCAGAGCCCCG TTAATGGGTG 120
 10 ATGGCGTGCC TTTTGTAGAA TGAACCGGCG AGTTACGATT TGATGCAAGG TTAAGCAGTA 180
 AATGTGGAGC CGTAGCAGAA GCACGGTTCT GGAATAGGGG CGTTTTAGTT ATTTTGGGTC 240
 GTTACCCGGG AGnAAAAG 258

(2) INFORMATION FOR SEQ ID NO: 4596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4596:

25 CCTACCGCTG CAGCCGCTGG ATCTGCTGGA GTTGCAATTAG GATCTGCCCG TGCCGCACGT 60
 CTACTTCTCT TTTTCGGTCT ATTAGATGCT GGTTCAGCAA TTGCAACTAG CTCTGGTTTA 120
 30 TTTGAAGAAT GACGAACATC TTCTTGAATT TCCTTTAAAG TAGATGTCCT CCTGAACCAT 180
 TnCATTTGTTT AGTTGGGTAC ATTAATGcng TATTATCGAC ACTACATCA 229

(2) INFORMATION FOR SEQ ID NO: 4597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4597:

45 GCTCACCTTA GAATTCTCAT CTTGCACTCA CCTGGTGGTC GGTTTGGCGG GTAGGGTCAC 60
 CTATTTTCTA TCTAGCAGGC TTTTCTCGGC AGTGTGAAAT CAACGACTCG AAGnACAAT 120
 GGTCTTCTCC CCATCACAGC TCAGCCTTAA CGAGTACCGG ATTTGCCTAA TACTCAGCCT 180
 50 TACTGCTTAG ACGTGCAATC CAATCGCAGC CTTCGCCTAT CCTACTGnGG TCCCCCATC 240
 GATTAA 246

(2) INFORMATION FOR SEQ ID NO: 4598:

- (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4598:

10 AAGAAAATAA AGAATGCTAC AATTACGATT GCAATCAAAC CAAAGAACCA TAATGATGTG 60
 TACCAAGTGC TGCACCTTTA GTAATGACAA CGTTTAAACT TAGCAACATA ACTACTAGAA 120
 CAATTAGCCC TGCAACGTCA AATTTATGTG TATTGGTAAT TTCTGATTTC GTTTCAGGCG 180
 15 TCCCTTTGAT GAGTAGCATT GAAAGTACGG nAACGATGnG TTG 223

(2) INFORMATION FOR SEQ ID NO: 4599:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 219 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4599:

nTnTCACTGT TTGACCCGGT ACCGTGTCAG ATAATCCCGC ACGCAATGCA ATCGTTCGTG 60
 30 CAATGTTTTG GCCTTGTAAT CCTTCTGGAA AAGCCGTACC AACAATGACA TCTTCAATCA 120
 TATTCTTATT GAATTTTCCG TCAATACGTT TCAATACGCC TTGTAATACT TTGGCTGCGA 180
 CATCATCAGG TCTTTCGTGG AATAATGCGC CTGCTTTGCG 219

35

(2) INFORMATION FOR SEQ ID NO: 4600:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4600:

AAGGTAAAGA GGAGTGTTA GCTTCTGCGA ATACCGAATC GAAKCCCCAG TAAACGGCGG 60
 CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCTTGTC GGGTAAGTTC CGACCCGCAC 120
 50 GAAAGGCGTA ACGATTTGGG CACTGTCTCA ACGAGAGACT CGGTGAAAAT CATAGTACCT 180
 GTGAAGATGC AGGTTACCCG CGGACAGG 208

(2) INFORMATION FOR SEQ ID NO: 4601:

55

(A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4601:

10 AGTGCCAGTG ATTAAGTCA TTTTCAATA GATCAGGGAA GACTACCAAG CTTATGTTGA 60
 AGGACATCTT TTGGCGTTAC CGGTTGGGCA GGTATGTTGT ATTACCGTTC ACAACAGCAT 120
 CACTTGAACA ACATTTGTTA ACGGATTATT TGGCAATTCG TTATTGTCTGA ACATGCTAG 180
 15 TTGGTGAGAT TTAATCATCG CTAAAGATGT GAAATAGATC GAAAATGGTT TAAGCAAACG 240
 TTGCTCAGGT GTTACTACGT GATATGCCTA GCGAGTATAC TACAAC 286

(2) INFORMATION FOR SEQ ID NO: 4602:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4602:

30 ATATGGCTAT GGTATTCACA TATCGATnAA CATGGACATA ACTCATGCTG GGTTTCCCCA 60
 TTCGGGAAAT CTCTGGGATC AAAGCTTACT TACAGCTCCC CAAAGCATAT CGTCGTTAGT 120
 AACGTCCTTC ATGGCTTCTA GTGCCAGGCA TCCACCGTGC GGCCTTAATA ACTTAATCTA 180
 35 TGGTTCCACC CATTTTTATA GGTCAAACGG TAACATGAGG TAGGGTCTTT TATAAAAAGG 240
 nTTAAACGGG GTATTAATCT TGTG 264

(2) INFORMATION FOR SEQ ID NO: 4603:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4603:

50 GAAACGTTAG CACAAGCCAT GAACCAATTA GGTGGAAAGA GTAATAGTGG TGAAGGTGGC 60
 GAAGATGCAA AACCGTTATG AAGTACAAGT TGATGGAAGC AACAAAGTAA GTGCGATTAA 120
 55 ACAAGTTGCT TCTGGGCGTT TTGGTGTAnC TAGTGATTAT TTACAACATG CCAAAGAATT 180

TATCCn

246

(2) INFORMATION FOR SEQ ID NO: 4604:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4604:

ATTAAC TAAC ATGGGCATCT ACGATGGAAA CAGACGTGGT ATCCTCGCTA TTATCCAGCT 60
AnCGCCATGC TGGCTCGTTT TTCAAATCAA GCCATTTTAA ATTTTGGAAG GGTGTATGGA 120
CCAAGCCCTA TGACATTGCA TTCACCGATT GAACACGATG TTATCGCCAT GTCTCATGGA 180
GAAAATCAAG AGCATCATTC AGCAGTATCG CGATGCTACA TTACGCGCGA TTAAAGCAGn 240
TTTGATGG 248

(2) INFORMATION FOR SEQ ID NO: 4605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4605:

CAAGTTTTCC AGTTTCCAAT GACCCTCCAC GGTTGAGCCG GGACTTnTCA CATCAGACTT 60
AAAAAACCGC CTACGCGCGC TTTACGCCCA ATAATTCCGG ATAACGCTTG CCACCTACGT 120
ATTACGCGCG CTGCTGGCAC GTATTAGCCG TGGCTTTCTG ATTAGGTACC GTCAAGATGT 180
GCACAGTTAC TTAACACATG ATGTTCTTCC CCTAAATGAA CAGAGTTTTG TTTTGTTTTn 240
TGGGTT 246

(2) INFORMATION FOR SEQ ID NO: 4606:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4606:

TGTATCTGCA GTTAAATCAT GTnTCGCTTG GTTTAATGCT GTTAATGCGT TATCGACACG 120
 ATGTTTTTCA TCTGAAATTT GTTGTGCAGT TGCATCGCCA TTGTCAATAA CACGTTGAGC 180
 5 TGCAGTTATT TCAGTTTCTG CTTACGCTn CT 212

(2) INFORMATION FOR SEQ ID NO: 4607:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4607:

TAGTCAAGAT GAGAATTCTA AGGTGAGCGA GCGAACTCTC GTTAAGGAAC TCGGCAAAAT 60
 20 GACCCCGTAA CTTCGGGAGA GGGGTGCTCT TTAGGGTTAA CGCCCAGAAG AGCCGCATGA 120
 ATAGGCCCAA GCGACTGTTT ATCAAAAACA CAGGTCTCTG CTAAACCGTA AGGAnTGTAT 180
 AGGGGCTGAC GCCTGCCCCG TGCTGGAAGG TTAAGAGGAG TGGTTAGCTT CTGCGAGTAC 240
 25 GGAATCGAAG CCCAGTAAA CGGCGG 266

(2) INFORMATION FOR SEQ ID NO: 4608:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4608:

TTCAGTACGT AAATACGCAC GTGAAAAAGG TGTTAnATTA AAGCAGTTTC TGGATCTGGT 60
 40 AAAAATGGTC GTATTACAAA AGAAGATGTA GATGCATACT TAAATGGTGG TGCACCAACA 120
 GCTTCAAATG AATCAGCTGC TTCACTGACA AGTGAAGAAG TTGCTGAAAC TCCTGCAGCA 180
 45 CCTGCAnCAG TGAACATTAG AAGGCGACTT CCCAG 215

(2) INFORMATION FOR SEQ ID NO: 4609:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GGGTTTCATAC ATGTCAATAG TAACCGTCTT AACTTGTTGT CGATTTTTTTA AATCGAATCG 60
 CTCGAAATAG GCACGCAAGA ATCTTGTAAGT TCTATTTTCT AAAATATCTA TAACATCATG 120
 5 GTATCATTAT CTATAAAAAT GAAACTCATT GATCCAGTTA CATTTTAAAC GCTTTTAAAT 180
 TCATCCATAG CGATGTGGTT CCTGCCAACC ATTAAAGGGG TTAATTCnGA ATnGATTAGC 240
 10 C 241

(2) INFORMATION FOR SEQ ID NO: 4610:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4610:

ATTCATTTCT TGTCTAGCAA CGTTCTACTC TAGCGGAACG TAAGTTAGCT ACCATCCTCG 60
 CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC 120
 25 TTAATCATT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 180
 TTTCAntTCG CCAAGCCATT TTTCTTTGGT GnTTA 215

(2) INFORMATION FOR SEQ ID NO: 4611:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4611:

GTGCCATCTT TCTTCATCAA TTCATTAATA ATTGCTGGGA CGCCACCAGC TTCATGCACA 60
 TCATGCATTG AATACGATGA ACTAGGTGCT ATTTTGGATA AATATGGCGT GCGTTTGGCA 120
 ATAGCATTA TCGCTCTAA GTCATAATCA ATACCAGCTT CATTGGCAAT GGCTAACGTA 180
 45 TGCAGTACCG TGTTTGTGA ACCACGGCAC ATCTTCGCCA ATTTCTTCTT TAAACAAGTT 240
 TAAATTATCT TGTGATTGAG GTAAATCCAT CTGTGTAAGT ACTACGATTT GAGGTCTATC 300
 TTCTAAACGT TGCTCGTACG GCGGCTAATT CTGGATTAAT GACTTTATAA TCTTCAATAG 360
 50 GGTCTCTACC TTCAGAACCG CTCCATATCC ATCCTGTGGA 400

(2) INFORMATION FOR SEQ ID NO: 4612:

(A) LENGTH: 258 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4612:

10 AATACTATTA AGAAGTCCTG AAAAATTCAC ATTAGCAGTT GGATTGTTCA ACTTTATTAA 60
TGATAAGTAT GCAAATAATT TCACAGTGTT TGCAGCAGGG GCAATTATGA TTGCAGTACC 120
TATAGCAATC GTATTCTTGT TCTTGCAACG CTATTTAGTA TCAGGTTTAA CAACAGGTGC 180
15 CGACCAAAGG GTTAGTTTGA ATTTAGGAGT GGGGCCAGAT TGGTTAAGGA CCnCTAATG 240
ACCGTTAAGG TTnAAAGG 258

(2) INFORMATION FOR SEQ ID NO: 4613:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 210 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4613:

30 GACTTCGTTT CAGTGTA AAA TTTTCTAAT GTAACAGATA TGCTATTATT CATTGGAATG 60
ATTAGTGCTT CATCTTTTTT ACCCCAATAT TTTATAAGTG CAATTCGTAT GTGCACGTGC 120
TTTGCCACTT TTAATCAACG CTTAACCTCC TAAATTCTCA ATCCAAGTAT GTGCTGCACC 180
35 AGCTTTTTTTC TACAGCTTTT ACAATATTnn 210

(2) INFORMATION FOR SEQ ID NO: 4614:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4614:

TAGCGTATTA ATCGGCCGAT CGGCTGAGCG TATCTGAGTC TGAATCGCTG TCTGAGTCTG 60
50 AGTCGTATCC GAGTCTGAGT CGCTGTCTGA nTCTGAATCA CTGTCTGAAT CCGnATCGCT 120
ATCTGAATCT GAATCGCTAT CCGAGTCTGA GTCGCTGTCT GAATCTGAAT CGCTGTCTGA 180
55 GTCCGAATCG CTATCTGAAT CTGAGTCGCT GTCTGAGTCT GAATCGCTAT CTGAA 235

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4615:

ATGTGCGTGG TTTATTTTAA TAGGTTAGTA ATATATTAGG TCATGTTATG TTAAAnTTTA 60
 TAATGAATAA ATAATTTAGA AATATGCTTC CGATTGTTTCG ATGCTTTAAT TCAGTTAGAA 120
 GCATCATAGA ATGCATGATT ACTGTTGTAA AGATACGTAA TGTTTTGTAT TGA CTGTATG 180
 TCnTTGGATA GAGTTACAAA CTTATTTTG 209

(2) INFORMATION FOR SEQ ID NO: 4616:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4616:

ATGCGCAAGA TATGGAGAAC ACCATCGCGA AGCGACTTTC TGGTCTGTAA CTGACGCTGA 60
 TGTGCGAnAC nTGGGGATCA AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT 120
 GAGTGCTAAG TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGCTAACGCA TTAAGCACTC 180
 CGCCTGGGGA GTACGACCGC AAGTTGAAA CTCAAAGGAA TT 222

(2) INFORMATION FOR SEQ ID NO: 4617:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4617:

CAGTTTGCAA CACCCCAATT CTTGCCAGTC AGCATGATTC TGTTCATTTT TGCGATTTCT 60
 TTGTCGATAT TTTCAAATCT TGTTGGACTT GATCTAAATC AATTGGTGCT TCTTCTTCGA 120
 ATGTATCAAC ATATCGCGGT ATGTTTAAAGT TGTAATCGTT ATCGGnGATC TCTTGTAATG 180
 TCGCGCTGTG GCTATATTTA TCAATCGTGG CTTTACGCTT ATATGGGGCT ATAATACGTT 240

(2) INFORMATION FOR SEQ ID NO: 4618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4618:

TCTAATTGAT AGTGAATATA ATTAGAGTTh GAGGCTGGGA CATAAATCCC TAAATTTCAh 60
CAGTAAGATA ATTTTCAATT AGAAAATATC TTAGTGCTGT TCTCTATTTA TACAATACTT 120
CATTGGAATG GCTTCGCTTT CCTAGGGTGC CGTCTCAGCC TCGGTCTTCG ACTGGGCACT 180
GCTCCCTCAG GGGTCTCGCC ATTAAATACT ACGTAT 216

(2) INFORMATION FOR SEQ ID NO: 4619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4619:

ATGTATCGCG CCGAGCAACA CAAGATAAGC ATTGTAGATG TGGATGCCTT AACTGGGCAA 60
GCGATThGTC GTCCTAAAC AGGTACATAT GCGCTATCTG ACCTAGTCGG TTTAGATATT 120
GCAGTGTCTG TAATTAAAGG CATGCAACAA GTACCTGAAG AAACACCCnT ATTTTCATGA 180
TGGTCAAAAT TTGTAAATAC GTTGTThTGA CAATGGGCGC ACCTCGGACC GTAAAACG 238

(2) INFORMATION FOR SEQ ID NO: 4620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4620:

AACCATTGAA GCACCCCAATT ACGTTTTGGC TGACACGhAC GTATATCGCC TGCCCAAGCA 60
GATGCAGCCT TATTAACACC TGAACCACTT CGAACGCCAC TACCTTTAAG TGACTTCAAC 120
CATTTTTCTT GGATCTTTAG CTGTATGCAT TGCCCTGGAT GCGACCCCTG nCATCAATTG 180

TTGACCAGC

249

(2) INFORMATION FOR SEQ ID NO: 4621:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4621:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCA AGAAAGAACG 60
TAAATTTAAT CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG 120
TGAGAAGACA ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA 180
AGGTGAATCG AAGAGAAATC ACAAAGTCCG TTnTGGnTTA CAGGTACGGC AGAACGATAC 240
ACAGTCTCGG GCGATTGTCTG AGTCCAC 267

(2) INFORMATION FOR SEQ ID NO: 4622:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4622:

CAAAAGGTAG TTAAATTAG GAGTGGGGAA ATTGATAAGA CCACTAATGA CGATAAAGAT 60
TAAAAGGAnG ACGTTATGAT GACGATTAAA GTTGATCAT TGGGTGTGGT GGTATTCCAA 120
TGGCAAGCAC ATGCCAAGTT TACAAAAAGT TGAAATGTTG AAATGAnCGC ATTTTGTGAC 180
GTAGACATTT CGAAGCAGCG AGTGCGGCAG AAGCATACGG ACTGACAATG C 231

(2) INFORMATION FOR SEQ ID NO: 4623:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4623:

CGAAACCGGC CCGACCCGGA CnACCCGAG GAAAGGTACC CnAAAGnTGA AGCCCGGGAA 60

CCCAACACCC ACCCGGACAC CAGAAGTGCC GGAGTGAGCC AGAAACTCCA ACACCGCCAA 180
 CACCAGAGGT ACCAGCTGAA CCTGGTAAAC CAGTACCACC TGCCAAAGAA GAACCTAAAA 240
 AGCCTTCTAA ACCAGTGGA CAAGGTAAAG TAGTAACACC TGTTATTGAA ATCAATGAAA 300
 A 301

(2) INFORMATION FOR SEQ ID NO: 4624:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4624:

CGAGGTGCTG CAGAAGGTGT CATTCGTCGT TATTTAATTG AAGAAAAGAA CTACTTAGAA 60
 GCTGTGATTG GTTGGCCAGC GAATATTTTC TATGGGACAA GTATTCCAAC ATGTATTTTA 120
 GTATTTAAAA AATGTCGCCA ACAAGACGAC AACGTACTAT TTATCGATGC ATCCAATGGT 180
 TTTGAAAAAG GGGnAAATCA TAATCATThG GCGATGCCCA AG 222

(2) INFORMATION FOR SEQ ID NO: 4625:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4625:

TGGAAAGTGA ATCAAAGAGG TAATATCCGT AGTCGAAATG TTGTCTCTCT TGAGTGATC 60
 CTGAGTACGA CGGAGCACGT GAAATTCCGT CGGAATCTGG GAGGACCATC TCCTAAGGCT 120
 AAATACTCTC TAGTGACCGA TAGTGAACCC AGTACCGTGA GGGAAAGGTG AAAAGCACCC 180
 CCGGAAGGGG AAGTGAAATT AGGAACCCTG AAAACCCGTG TGCTTTACCA AAGTTAnGTT 240
 CAAGAGGCCC CGTTTAAATT GGGGThnAAT TGGCGGTGCC CTTTTTTGGT AGGAATTGAA 300
 A 301

(2) INFORMATION FOR SEQ ID NO: 4626:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4626:

5 GAATGAAGGA AGACCATATG AAAAATGGCC AACTTAAGCC AGGATACAAT TTACAAATAG 60
 CGACAAATTC TCAATTTGTT TTATCCTATG ACCTATTTCA AAACCCAACA GATACTAGAA 120
 10 CATTAAATCCC ATTTTTCATCA ATGATTCAAA ATACCTTCGG TTATTTACCA GAGTATATTG 180
 TAGCTGATGC AGGTTATGGT AGTGAGCAAA ACTATATGGC nAT 223

(2) INFORMATION FOR SEQ ID NO: 4627:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4627:

TTGTTGGGGC CCCGCCnGCG nCATTGCCTG TAGAATTTCT TTTGAAATT CTCTGTGTTG 60
 25 GGGCCCCTGA CTAGAATTGA AAAAAGCTTA TTACAAGCGC ATTTTCGTTC AGTCAATTAC 120
 TGCCAATATA ACTTCGTAGA TCATAGAACA TTGATTTATT TCCCAGCCTA TTCTTTTCAT 180
 30 AAAAAAAGA CGGATTAATT ATCCGCTTTT TCCTTATATC T 221

(2) INFORMATION FOR SEQ ID NO: 4628:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4628:

ATATATTCGT ATTTATAGTA AAATTAAATA AAGAGnATTA TATAACACGA GGTGTAGTAA 60
 GTATGAAATT TGAGnAAATA TATAGATCAC ACTTTATTGG AAGCCTGAGT CAACACGTAC 120
 45 GCAAATCGAT CAAATCATCG ATGAAGCGAA GCATACCAAT TTAAATCTG TATGTGTGAA 180
 TCCACCACAT GTTAAATATG CAGCAGAG 208

50 (2) INFORMATION FOR SEQ ID NO: 4629:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4629:

5 ACAATAATGC ATCATAATGC GCAACAACAA TCAATACTGC GAAAACAGAA GCACAACAAG 60
 TGATTAATAA TGAGCGTGCA CACCACAACA AGTTTCTGAC GCACTAATAA AAGTTCGTGC 120
 ACACAACTAA GATTGATCAG CTAAAGCTTA CTTCAAAATA AAGAGATATA GCCATTAGTA 180
 10 ACGTTAAAAA AACTTACAAG nTCTGTGACC AGTACCTCAC TGTGGTATGA CGCACAAGTA 240
 TTGATACTnT ATCGAGAGCG TGAGnGAACT GAATACTGCG CTCACGGTAT TACATGCGTG 300
 CACTG 305

15 (2) INFORMATION FOR SEQ ID NO: 4630:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4630:

TCGACTACCA TCGACGCTAA GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGTGTGACT 60
 CCTTGCTATA GTCACCAGAC ATATGAATGT AATTATACAT TCCAACTAG ATAGTAAGTA 120
 30 AAAGTGATTT GCTTCGCCAA ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT 180
 CAGCTCCACA TGTCACCATG CTTCCAnCTn GAA 213

(2) INFORMATION FOR SEQ ID NO: 4631:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4631:

45 GAnGTGAAAT AGAACCTGAA ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA 60
 TGGCGTGCCT TTTGTAGAAT GAACCGGCCA GTTACGATTT GATGCAAGGT TAAGCAGTAA 120
 ATGTGGAGCC GTAGCAAAAA CnAAGTTCTG AATAGGGCGT TTAGTATTTG GTCGTAGCCG 180
 50 GAAACCAGGT GATCTACCCT TGGTCAAGTT GAA 213

(2) INFORMATION FOR SEQ ID NO: 4632:

- (A) LENGTH: 205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4632:

10 GCTTTTAAAT CAAATGATAG CGGAAGGGnA TTTTAAAATT ATTCGAACCA TTATTTACAG 60
 CAGCAGATGG ATGGATTGGT GTCACAATTA TCTTTGGTGC CTTTGCATTA TTCTGGTTTG 120
 TAGGTATTCA TGGTCCGTCA ATTGTAGAGC CAGCAATTGC AGCCATTACA TATGCGAATA 180
 15 TCGAAGCGAA CTTCAAGTTG CTTCA 205

(2) INFORMATION FOR SEQ ID NO: 4633:

- (i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4633:

AGTTATATTG ACAGTAGTTG ATGGGGCCCC AACATAGAGA AATTGGAACA CCAATTTCTA 60
 30 CAGACAATGC AAGTTGGGGT GGGCTCTAAC ATAAAGAAnt ACTTTTTCTn TAGAAATTAG 120
 TATTTCTTAT ACATGGGTTT TACTCAGTAT TTCCTATTCT TAAGTGCACA TTAGCAGCGG 180
 CTAATGTGTT AAGAACTACT ACAT 204

35 (2) INFORMATION FOR SEQ ID NO: 4634:

- (i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4634:

GCCGATGGAT TAGAGTATAT GACGTGGTGG CATGTCATTA ATTTAGGTGA TGTAAGGTAAG 60
 AACGTTnGGG CAAGGTATGA GTGGTGGTAT TGC GTTACGT TAGCCCGTCT GATGTAGAAG 120
 50 CTTTTGTTGA AAATAATCAA CTAGATACGC TTTCGTTTAC AAAGATTAAA CACCAAGAAG 180
 AAAAAGCATT CATTAGCAA ATGCTGGAAG AnCCATGTGT CACACA 226

55 (2) INFORMATION FOR SEQ ID NO: 4635:

(A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4635:

10 CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA ATATACTCTG GTAAATAACC 60
 GAAGAGTTGT TGAATCATTG TAAAAATGG GATTAATGTT CTAGTATCTG TTGGGTTTGT 120
 AAATAGGTCA TAGGATATAA CnGTACGGAG AATTTGTCGC TATTTGTAAA TTGTATCCTG 180
 15 GCTTAAGTTG GCCATTTTTC ATATGGTC 208

(2) INFORMATION FOR SEQ ID NO: 4636:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4636:

TTTTTCTTTG TGTTTATTTT TATTTTGAAC GTTTTAGGAC ATAAAAAATA GTAGACCTTG 60
 30 CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA 120
 CGTAAGTTGG CTACCATCGA CGCTAAGAAC CTTTCTTGAC TTGTGACAAT CGCTTGCTTC 180
 TTTCCGCTTC TTCTGCTCGn GCTTACTCAT TGAGCnCTAC TAAACTCG 228

35

(2) INFORMATION FOR SEQ ID NO: 4637:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4637:

CATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCACCTATA GATGGATCCG CGCTGCATTA 60
 GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA TAGCCGnCTT GAGAGGGTGA 120
 50 TCGGCCACAC TGGAGCTGAG ACACGGTCCA GACTGCTACG GGAGGCAGCA GTAGGGnATC 180
 TTCCGCAATT GCGGAAAGCT GTACGGGCAA CG 212

55

(2) INFORMATION FOR SEQ ID NO: 4638:

- (A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4638:

10 ATnTnATTAA ATAGAGAACA GCAGTAAGAT ATTTTCTAAT TGAAAATTAT CTTACTGCTG 60
 TTTTTTAGGG ATTTATGTCC CAGCCATTTT TGTATTCATA TTAAATTTC GATAATTTTT 120
 CAGGAAGCAT TTTAATTTTA CTAATGAAGC CATATTTTTA GATTAACCAA AATTAATATT 180
 15 TACATTTTCT AACCATTTTT ATGTAACATT TACAGTTCCA AAAATGGGGG TAATAATCCA 240
 GGTTAGGATA AAGAGG 256

(2) INFORMATION FOR SEQ ID NO: 4639:

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4639:

30 AnAGnAACCA CTACATAATA AATCATTAGT GGCTCTTTAT CATTTCTGTC CCACTCCCCT 60
 GAGAAGTTTA AAATTTTATA TGTTGGCTTG TTATGTTAAG GGAATTAACA TGGTTGTCTT 120
 GTTTATATTA TGTGATTCCA ACATTACTAG TCCTGGTAAA TCTAATTCCG TAAAATGCTA 180
 35 AATCTAACCA TCTATTAAAT TTAAAAACC 209

(2) INFORMATION FOR SEQ ID NO: 4640:

40

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4640:

nGnAAAGGTG AAAAGCACCC CGGAAGGGAG GTGAAATAGA ACCTGAAACC GTGTGCTTAC 60
 50 AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA CCGGCGAGTT 120
 ACGATTTGAT GCAAGTTAAG CAGTAAATGT GGAGCCGTAG CAGAAGCATG GTCTGAATAG 180
 55 GTGCGTTTAG TATTTGGTCG TAGCCCGCAG AACCAGGGTG ATCT 224

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 205 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4641:

CACTCACHCA GATTTTAAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA 60
AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TTTATTCTAC 120
CGCTGAACTA CTTCTGCATA TCGGGGTGAA GGGAGTCGAA CCCCCACGCC GTAAGCTAng 180
ATCCTAAGTC TAGTGCGTCT GCCAA 205

(2) INFORMATION FOR SEQ ID NO: 4642:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 235 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4642:

AGCTGACATG ATCAGTCAGC TTACAACAAT GTGCCGGTTG GGGTGGCTGG ACACGGCACC 60
CTGAGGGAAG GGCACCCGTC ATCAAAATT CTATTTATAG AATTTTACAG TAATGTGACA 120
GACGGGCAAA GCGAACCATT CAATACGAAG TATTGTATAA ATAGAGAACA GCAGTAAGAT 180
ATTTTCTAAT TGAAAATTAT CTTACTGCTG TnTTTTTAGG GATTTATGTn CCCAG 235

(2) INFORMATION FOR SEQ ID NO: 4643:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4643:

AGnAAGGTGG GGATGACGTC AAATCATCAT GCCCCTTATG ATTTGGCTAC ACACGTGCTA 60
CAATGGACAA TACAAAGGCA GCGAAACCGC TAGTCAAGCA AATCCCATAA ATTGTTCTCA 120
GTTGATTGT AGTCTGCGAC TCGACTACAT GAAGCTGGAA TCGCTATAAT CTAGATCAGC 180
ATGCTACGTG ATAGTTCCGG GTCTnTACAC ACGCCCGTCA CACCACGGAG GGTTTTACAC 240

(2) INFORMATION FOR SEQ ID NO: 4644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4644:

CAGCAGGCCA CCAAAATTGT GGTCCGAGAT GTTCATATAA AACTTTATAT AATTCATCAG 60
 TTCCTAACAT TTACACCCTC CATTTTAGAG GGAGTGGGAC AGAAATGATA TTATCGTAAA 120
 ATTTATTTTCG TCGTCCCACC CCAACTTGCA TGTCTGTAGA AATGGGGATC CAATTCnCTT 180
 GTTGGGGGCC CGCGGGCAAG GTnACTAGAA TGAAAAAAGC CTGTTACAAG CGATTTTCGG 240
 TTCAGTCCAC TACTGGCAAT ATAACCTGTA GAGCTAGGAC ATTGG 285

(2) INFORMATION FOR SEQ ID NO: 4645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4645:

GCTATTACTC TGCTATCAAT GTACCTAAAG CTACCGATGA TTTCCGAGAC ATAGACCGTG 60
 CGCTTGnTG GGGGTTCAAC TGGAACTTG GTCCATTCCA ATTATGGGAT GCAATGGGGn 120
 TACGAACGTG TAAAACAGT ATGGAAGACG AACTTGAGA CTTACCACAA TGGGTTAGTG 180
 ATTTAGATGG TGGCTTTTGA TAAACA 206

(2) INFORMATION FOR SEQ ID NO: 4646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4646:

ACAGTTACCG ATACAACTGA AGATGATAAC GATGCAGATG GTGGCGACGT TGACGTCACA 60
 CTTACGGATC ATGATGATTT CAACTTGAT AACGGATACT TCGAGATGAT ACATCAGACA 120

CnGACAGTGA TTCAGATTCA GACAGCGACT CAGATTcNGA TA

222

(2) INFORMATION FOR SEQ ID NO: 4647:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 200 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4647:

GTACTATTCG TGTGTGACAA TGTTCTTCCA GCATTTGCTT AATGAATGCT TTTTCTTCGT 60
 TTAATCTTTG TAAACGAAAG CGTATCTAGT TGATTATTTT CAACAAAAGC nTCTACATCA 120
 GnCGGGATAA CGTAAGCAAT ACCACCACTC ATACCTTGAC CGAAGTTCTT ACCTACATCA 180
 CCGAAATTAA TGACAGTCCA 200

(2) INFORMATION FOR SEQ ID NO: 4648:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4648:

CCACCATTAA TTTAATACCT ATTTGGGGGC TTAGCTCAGC TGGGAGAGCG CCTGCTTTGC 60
 ACGCAGGANg TCAGCGGTTT GATCCCCTA GTCTCCACCA TTATTTGTAC ATTGAAAAC 120
 AGATAAGTAA GTAAAATATA GATTTTACCA AGCAAAAACCG AGTGAATAnA GAGTTTTTAA 180
 TAAGCTTGGA ATTCATTAAG A 201

(2) INFORMATION FOR SEQ ID NO: 4649:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 218 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4649:

AGTAAATACA GATGGAATAA ATCTTTTAAG GCTTATAAAC GCTCATCTGn CATTGTAGCA 60
 ATTCATGCTT TCAAAAGACG ATATACTACG ACACTCCTAC GAACTTGTCC AAGGATTACG 120

AAAGTCTGTG AGTAAGGGTG TATGGAAAGT GGTnAAAT

218

(2) INFORMATION FOR SEQ ID NO: 4650:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4650:

GTGGCGGTGC GACTGTCAGA AGCACGTTAA ATTAATGAAA GATACAGTAG GTGCTGATGT 60
 AGAAGTAAAA GCCATCAGGT GCGGTACGTA ATTTAGAAGA TTTCAATAAA ATGGTTGAAG 120
 CAAGTGCGAC ACGTATTGGT GCGAGCGCAG GTGTTCAAAT TATGCAAGGT TTAGAAGCAG 180
 ATTCnGATTA CTAATATnTA TG 202

(2) INFORMATION FOR SEQ ID NO: 4651:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 209 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4651:

AGCGGCGGAC GGGTGAGTAA CACGTGGATA ACCTACCTAT AAAACTGGnA TAACTTCnGG 60
 AAACCGGAGC TAATACCGGA TAATATTTTA AACCGCATGG TTCAAAGTA AAAGACGGTC 120
 TTGCTGTCAC TTATAGATGG ATCCGCGCTG CATTAGCTAG TTGGTAAGGT AACGGCTTAC 180
 CAAGGCAACG ATGCATAGCC GACCTGAGA 209

(2) INFORMATION FOR SEQ ID NO: 4652:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4652:

TGAAGATGCA GGTTACCCGC GACAGGACGG AAAGACCCCG TGGAGCTTTA CTGTAGCCTG 60
 ATATTGAAAT TCGGCACAGC TTGTACAGGn TAGGTAGGAG CCTTTGAAAC GTGGAGCGCT 120

CCACTTATCG TGGTTGGAGA CA

202

(2) INFORMATION FOR SEQ ID NO: 4653:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4653:

CCGTGCGACC CCTTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC GTTCCCGGTA 60
 TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGCTCT 120
 ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG 180
 AACCGGTACG TGATCACTCA ACnGn 205

(2) INFORMATION FOR SEQ ID NO: 4654:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4654:

AGACGAAACG TTGTTGTTGC GAAGATAAAT CGCACAGCGA TTGAGCCTAT CTGCTGCACC 60
 ATTAAGTGGT GAAGTAACAC CATTATCAGA AGTGCCTGAT CAAGTGTTCA GCGAAAAAAT 120
 GATGGTGACG GTATCGCTAT CAAACCTTCA CAAGGTGAAG TTCGTGCACC ATTCAACGGT 180
 AAAGTACCAA TGATTTCCTCA ACCAAACATG CCATTGGTCC TGTATCAGAT AGTGGTTAGn 240
 CTATTAATCC ACACGGGTTA GAnG 264

(2) INFORMATION FOR SEQ ID NO: 4655:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 211 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4655:

GACGATTACA TATCATCGCT AATAACTTAG CATTAAAACC GCTTGATGCG CCACCACAAG 60

AACACAACGA ACTGGGnACA TGCTTCGGTT AAATCCATCA ATTTCAACGC TTGTnACGCG 180
 AAATCAGTTT GCTCTTGGCT GCAGTAAATC G 211

(2) INFORMATION FOR SEQ ID NO: 4656:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4656:

TTTACATTTA TCGGTTTAGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC ATCTTTCTTT 60
 GTGTTTGCTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTTGCGG TCTCAATGCG 120
 GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTCGACT 180
 ACCATCGACG CTAAGGnGCT TAACTGnTGG GT 212

(2) INFORMATION FOR SEQ ID NO: 4657:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4657:

TGGGTTTCGAA nTCCACTTAG GACCCACCAT TAACTTAATA CCTATTGCGG GGCTTAGCTC 60
 AGCTGGGnAG AGCGCCTGCT TTGCACGCAG AGGTCAGCGG TTCGATCCCG CTATCTCCAC 120
 CATTATTTGT ACATTGAAAA CTAGATAAGT AAGTAAATA TAGATTTTAC CAAGCAAAAC 180
 CGAGTGAATA AAGAGTTTTA 200

(2) INFORMATION FOR SEQ ID NO: 4658:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4658:

TACAGTATAT CGGGAAGACA GGATTCTGAAC CTGCGACCCC TTGGTCCCAA ACCAAGTGCT 60

CTCTTGATCC GTAGTCAAAC GCTCTATCCA ATTGAGCTAC GGGCGCATAT GTTTTATTG 180
AAAAan 185

5 (2) INFORMATION FOR SEQ ID NO: 4659:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4659:

AAGTGTTAGG GGGTTTCCGC CCCTTAGTGC TGCCAGCTAA CGCATTAAGC ACTCCGCCTG 60
GGGAGTACGA CCGCAAGTGT ATAACTCAA GGAATTGACG GGGACCCnCA CAAGGTTGGA 120
20 GCATGTGGTT TAATTCGAan CAACGCGCAG TAACCTTACC AAATCTTGAC ATCCTTTGAC 180
AACTCTAGAG ATAGAGCCTT CCCCTTCG 208

(2) INFORMATION FOR SEQ ID NO: 4660:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 365 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4660:

35 ACGTCGCGAG AACGCAATTA GCTGAAAAAG ATTACAACAT TAGAACAAGA TTAAAGTCA 60
CATTTAGTGA ACATCAAAGG CCGAATAACA TCATAAATTA CGATTAGATA TAACAAAAGA 120
GCTTGGGACA TAAGTCCTAA AGTCTTAGGC AAGTAAAAAA GTGATTTCTA TTATTTATTT 180
40 GATAGAAATC ACTTTTTGAT ATGTATTTnT ATGTACAGCT CGTTGAGCnC TATTTTCCTT 240
ATATTAGTGC CATAATACAA ACCTAGCTCT TGTTTAACTT TATTATTCCG AACTGACATC 300
GGTGAACCCA ATAGCCTCAT AAGCAAACAG CTTACATCAT TTTCTTGAnT GGTTTTCGTT 360
45 CTGTC 365

(2) INFORMATION FOR SEQ ID NO: 4661:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4661:

AAAGTATTTTC TTTATGTTGG GGGGCACCCC ACTTTGnCAT TGTCTGTAGA AATTGGGAAT 60
 5 CCAATTCTCC TnATGTTGGG GCCCGCAGT TCAACTACTG CCAATATAGT GTTGTAGTGT 120
 CTAAGACATA AAAGTTCATC TCAGTCACAA TTA CTTTATA GCCTATCCAT CATCTTTTCT 180
 ACATGAAATT TTTCCAAGTG ATATATTTT 209

(2) INFORMATION FOR SEQ ID NO: 4662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4662:

TTATGGCACT TAAAACCAGC GATGACGATT GCAGTATCAC ATGGTATCTT CAACATAACA 60
 AATACTTTGA TTCAATTACC ATTTGTAGCA GGTTTAGCAT GGATTGTTAC AAAGCTTGTC 120
 25 CCAGGTAAAG ATATTGCTGA TGA CTTATAAA CCTCAGCACT TAAACCAAGG TCTGTTATCA 180
 CGCACCTGGT GTTTGCATAC CAGGAACTCC AAAAGGATTA CCAAATGTnG GGGCAGAnTG 240
 GCCTAA 246

(2) INFORMATION FOR SEQ ID NO: 4663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4663:

AATGGTGTAT TATGAGTAGT AATAATTAGC AAAGAGGTAA ATTAAGTGAT GTCGCGTCAT 60
 TTAAGGAAGC GATTCACAAT CGAGAATCAC AAAGTACAAC TGGTATCGGC GAAGGTATnG 120
 45 CCATTCCACA TGCCAAAGTG GCCGCAGTTA AGTCACCAGC TATTGCGTTT GGTAAATCTA 180
 AAGCAGGCGT AGATTATCAA AGnTTTGGT ATGCAACCAG CACACT 226

(2) INFORMATION FOR SEQ ID NO: 4664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4664:

5 TTCCGTCTCG GCACCATTTT AGCGCCGTAG CTCAATTGGA TAGAGCGTTT GACTACGGAT 60
 CAAGAGGTAT GGGTTCGACT CCTATCGGGC GCGCATTTTT AAATTAATTG AATAACGGGA 120
 GTAGCTCAGC TTGGTAGAGC ACTTGTTTGG GGACAAGGGC GCAGGTTCTGA ATCCTGTCTC 180
 10 CCGATTACTT CTAAATCCAT TTATGGGGCT ACTCACTGGG nACGCCTCTT nCAC 234

(2) INFORMATION FOR SEQ ID NO: 4665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4665:

GTACATCTAA AATCATCCAT GAAGGTTTGT TACCTGAATT ACGGAATGAT TCAACAACTT 60
 25 CTAAACGTTT AATTnACCAG TAAGTCTTTG CCAAGTAGCT GATTCCAAC CATCGCGTAC 120
 AATTTAAGTC TTCGTCAAGA TCAATCCTCT TCAAGTAAAT CTTTAATAAC CTTCTGCACC 180
 30 CATTTTTGCA CGAATT 196

(2) INFORMATION FOR SEQ ID NO: 4666:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4666:

CCGCCGAACA ACTACTTTGT TTGTTGATTC TCTCCACCTG TTTCAGTAGT TCAGATTTCT 60
 TAGATTGTGG TTTTITAGTT GGTGCCATGC TTAAACCTTT TCATTGATTT CAATAACAGG 120
 45 TGTTACTACT TACCTGTTCC ACGGTTTAGA AGGCTTTTAG GTTCTTCTTG GCAGTGGTAN 180
 GGTTTACCAG TTCAGCGGTA CCGCGGTGTT GGnCGTGTG GATTTT 226

(2) INFORMATION FOR SEQ ID NO: 4667:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4667:

5 GTTCTGAATA GGGCGTTTAG TATTTGGTCG TAGCCGAnAA CCGGTGATCT ACCCTTGGTC 60
 AGGTTGAAGT TCAGGTAACA CTGGAATGGG AGGACCGAAC CGACTTACGT TGAAAAGTGA 120
 GCGGATGAAC TGAGGGTAGC GGAGAAATTC CAATCGAACC TGGAGATAGC TGGTTCTCTC 180
 10 CGAAATA 187

(2) INFORMATION FOR SEQ ID NO: 4668:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4668:

CTAAGTGGAG TTGTCACAAC ATCTTTAAAC GTTCCAGGTA AATAGTCTTT TGCCATTTCT 60
 25 GAAAATGCTT TTGCCAACGT TTTATAAATA TCCCAGTCTG AACGCGATTC CCATAACGGA 120
 TCAATGGCAG GATTGAAAGG ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGn 180
 30 TT 182

(2) INFORMATION FOR SEQ ID NO: 4669:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4669:

AGTTACGTTA AAAGATGAAA ACGACAAAGT TTTAAAAACA GTTACAACAG ATGAnAATGG 60
 TAAATATCAA TTCACTGATT TAAACAATGG AACTTATAAA GTTGAATTCG AGACACCATC 120
 45 AGGTTATACA CCAACTTCAG TAACTTCTGG GAAATGATAC TGCAAAAAGA TTCTAATGGT 180
 TT 182

50 (2) INFORMATION FOR SEQ ID NO: 4670:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4670:

5 GGGGCAAAGT CATThCATAG ATTAATGGTT CTCCGATACC TAGGAAACCA ACTGGCAATG 60
 CACCTTTTAA AGTATTACGT AATGTTGTGT TGC GTTTACA TCTTACCCAA AGTGCTAATG 120
 10 CGGCACCTAC TTGTCCAGCA CCAGCCATCG CTGCAATTGG CAATAAGTAA GTAGCACCTG 180
 ATTGG 185

(2) INFORMATION FOR SEQ ID NO: 4671:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4671:

25 CTGACGAACG AGAAAAGAGC GCAACGATTT AGTAGAGTAA ATGAGTTAAG CGAGACCGAA 60
 GAAGAGGAAA GAAGCAAGCG ATTGTCACAA GTCAAGAAAG GTTCTTAGCG TTCGATGGTA 120
 GCCAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAA AAAAATGGAT GCGATGACCG 180
 30 CATTGAGACC GCAAGGnTnT 200

(2) INFORMATION FOR SEQ ID NO: 4672:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4672:

CCCGGGGTAC AGTTATTCCC CAGAGTCAAC GCGGGGGTTG GACTCGATGT CGGTCATCGC 60
 45 ATCCTGGGCT GTAGTCGGTC CCAAGGGTTG GGCTGTTTCGC CATTAAAGCG nACGnTGCTG 120
 GGTTCAGACG CGTGAGCAGT CGGTCCCTAT CCGTCGTGGG CGTAGGAAAT TTGAGAGGGC 180
 TGTCTTAGT ACGAGAGGCC GGGATGGCAT ACCTTGGTGT ACCATTGTCTG TGCCACGCAT 240
 50 AGTGGGTAGT ATGTGTGGAC G 261

(2) INFORMATION FOR SEQ ID NO: 4673:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 184 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4673:

10

ATAGGGCGTT TAGTATTTGG TCGTAnCCAG AAACCAGGTG ATCTACCCTT GGTCAGGTTG 60
AAGTTCAGGT AACACTGGAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA 120
ACTGAGGGTA GCGGAGAAAT TCCAATCAAA CCTGGAGATA GCTGGTTCTC TCCGAAATAG 180
CGTT 184

15

(2) INFORMATION FOR SEQ ID NO: 4674:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4674:

30

CCCAGTCAAA CTGCCCCGCT GACACTGTCT CCCACCACGA TAAGGTCGTG GGTGAGAAA 60
GCCAACACAG CTAGGGTAGT ATCCCACCAG CGTnCTCCAC GTAAGCTAGC GCTCACGTTT 120
CAAAGGCTCC TACCTATCCT GTGACAAGnT GTGCCGAATT TCAATATCAG GCTACAGTGA 180
AAGCTCCACG GGGTTCTTTC CGT 203

35

(2) INFORMATION FOR SEQ ID NO: 4675:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4675:

45

nnGTTTGTAA ATAATATGGT GGAGACTAGC GGGATCGAAC CGCTGACCTC CTGCGTGCAA 60
AGCAGGCGCT CTCCCAGCTG AGCTAAGCCC CCATAATAAT TACAGTATAT CGGGAAGACA 120
GGATTCGAAC CTGCGACCCC TTGGGTCCCA AACCAAGTGC TCTACCCAGC TGGAGCTTAC 180
TTTCCCGGTA TTATTTAACG CGGCCCGATA GGGAGTCGGA ACCCATTA 229

50

(2) INFORMATION FOR SEQ ID NO: 4676:

55

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 178 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4676:

TCTAAAAATC GCGCACTTAA ACCGCTTATG ACAATCATTG TTACCTCAAT ATGCTTGTCA 60
10 TCACTTGCCT TTATCGTCGT TCATTGGCTA TATAGTTAAT ATGAAAAGAC GCTCAAACAC 120
TTACAAATTT AGTGTGCnGA GCGTCTTATT TTTATACTTT AAAAGTCGTA TTGGTTGT 178

(2) INFORMATION FOR SEQ ID NO: 4677:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4677:

GCAAGTAAGC ATAATGTGGA GCCGTAGCGA AACAGTCTGA ATAGGGCGTT TAGTATTTGG 60
25 TCGTAGACCG GAAACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG TAACACTGAA 120
TGAAGGACC GAACCGACTT ACGTTGAAAA ATGAGCGGAT GAACTGAAGG TAACCGGAGA 180
30 AAATCCCAAT CGAACCCTGG GAGATAAGCT TGGGnTCTCC TCCCGAAAAT AAGCCTTTTA 240
GGGGCTTAAG CCTCCAAAGT GGATGATTGA ATTTGGAAGG TAAAn 286

(2) INFORMATION FOR SEQ ID NO: 4678:

35

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4678:

CACACGGCTT ATGGTAACAA AAAATTCCTT TGGAGCATTA TGGAGCGGAA GATAGGTTTA 60
45 CACCTATACC TCGTTCGGGA AGGAnTGTTT TAAAAGTGAA CTACTCCCGC AATATTAAAT 120
ATGGAGCGGA GATAGGATTT ACACCTATAC CTCATTCCAG AGGATGTATT CTAAGAGTGA 180
50 AATACTCCCC ATATATTAAA TATGGAGCGG AGATAGGATT GACCATACh 229

(2) INFORMATION FOR SEQ ID NO: 4679:

55

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4679:

ATGACTGCTT TTTATTATAC TTTACATTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT 60
CGCCAAGCCA TCTTCTTTG TGTTCGCTT TATTTTGACG TTTTAGACAT AAAAAAGAG 120
ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG TTC 173

(2) INFORMATION FOR SEQ ID NO: 4680:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4680:

AAAAGTAACA AGAGAAGGAC AAAAAGGTGA GAAGACAATA ACGACGCCAA CAAAAATCCA 60
TTAACTGGAG AAATTATTAG TAAAGGTGAA TCGAAAGAAG AAATCACAAA AGATCCCATT 120
AATGnATTAA CAGAATACGG ACCAGAAACG ATAACACCAG GTCATCGAGA CGAGTTTGAT 180
CCC 183

30

(2) INFORMATION FOR SEQ ID NO: 4681:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4681:

CGGTGCTTTC ACTTTCCTAC AGACTGGTTA CTATCGGTCA GAGAGAGATT TAGCnTTAGG 60
AGATGGTCCT CCCAGATTCC GACGAATTC ACGTGTTCG TCGTACTCAG GATCCACTCA 120
AGAGAGACAA CATTTTCGAC TACAGGATTA nTACCTTCTT TGATTCATCT TTCCAGATGA 180
TTCGTCTAAT GTCGTCCTTT GTA 203

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(2) INFORMATION FOR SEQ ID NO: 4682:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4682:

GGGTCACACC TGTTC CATG CCGAACACAG AAGTTAAGCT CCTTAGCGTG CGATGGTAGT 60
CGAACTTACG TTCCGCTAGA GTAGAACGTT GCCAGGCAAA AAGTGGGATG CGATGGAGCC 120
GCATTGGAGA CCGCAAGCCT CTGTTCTTTG ATGTCTAAAA CGTnCAAAAT AAAAGCGAAC 180
ACAAAGA 187

(2) INFORMATION FOR SEQ ID NO: 4683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4683:

GGCTACACTG GTCATGATGC TGCTAAACTA CGTGATTATn ATGAAACACA TCATGCTTTG 60
TCTGGATATG AAATGATTGA CGCAGCAAAG GTGCCATTGC AACAAATGAA GTCAATGCTG 120
CGATGGGTAT ATTTGTGCAA CGCCAACAAC TGGTTCCTCC GGTACCATCC CGGTGCAGTT 180
TTAAATT 187

(2) INFORMATION FOR SEQ ID NO: 4684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4684:

AGTGCCAAGG CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA 60
AACCGTTATT AATCTTGTGA GTGTTCTTTC GAACACTAGC GATTATnTCT TATGAATTCA 120
AGCTTATTTA AAACCTCTTA TTCACTCGGT TTTGTAAAAT CTATATTT 168

(2) INFORMATION FOR SEQ ID NO: 4685:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4685:

ACGGGAAGTA GCTCAGCTTG GTAGAGCACT TGGTTTGGGA CCAAGGGGTC GCAGGTTCTGA 60
 ATCCTGTCTT CCCGATTACT TCTTAAATTC CATTTTATGG GGGCTTAGCT CAGCTGGGAG 120
 AGCGCCTGCT TTnCACGCAG GAGGTCAGCG GTTCGATCCC GCTAGTCT 168

(2) INFORMATION FOR SEQ ID NO: 4686:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4686:

ATGATTCAAG CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT 60
 TTACTIONACTT ATCTAGTTTT CAATGTACAA TTTCTTTTTA GTCAAGCGCT CGCATACTGC 120
 nTTATTTTCA AAAAATCAAA TGCTCATTTA CAAAAGTAAA CTCCGCTTTT AATT 174

(2) INFORMATION FOR SEQ ID NO: 4687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4687:

TGTTGTTGAA TATGAAGAAG ATACAAACCC AGGTGGTGGT CAGGTTACTA CTGAGTCTAA 60
 CTTAGTTGAA TTTGACGAAG AGTCTACAAA AnGTATTGTA ACTGGCGCAG TGAGCGATCA 120
 TACCACAGTT GAAGGTACGA AAGAATATAC AACTGAAGTA ATCTGA 166

(2) INFORMATION FOR SEQ ID NO: 4688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4688:

AGAACCTTAC CAAATCTTGA CATCCTTTGA CAACTCTAGA GATAGAGCCT TCCCCTTCGG 60

GCAACGAGCG CAACCCTTAA GCTATTGCCA TCATTAAGTT GGGCATCTAA TTGACTGCCG 180
GTGACAAAC 189

(2) INFORMATION FOR SEQ ID NO: 4689:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 227 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4689:

TAACCACTCC TCTTAACCTT CCAGCACCGG GCAGGCGTCA CCCCTATACA TCACCTTACG 60
GTTTAGCAGA GACCTGTGTT TTTTGATAAC AGTCGCTTnG GGCTATTACAC TGC GGCTCTT 120
CTGGGCGTTA ACCCTAAGAn ACCCTTCTCC CGAAGTACGG GGGCATTTTG CGAGTCCTAA 180
CGAGGTCGTC GTCACCTAGA TTCTCATCTT GATACTGTGT GGTTCG 227

(2) INFORMATION FOR SEQ ID NO: 4690:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4690:

AGATAATGCA CCATCAACTA ATGGATATTT ATGTCCAGTT GGGGGCCAGA AATCATAAAC 60
GTCTTCAGTG TAAGCAACAG CATCTTCATT TnGCAGCCAA AATGCTTGGA TTATGTGCAA 120
TAACCATCGC AACTGCGCCA CACCTTGTGT TGGCTCGCCG CCTGAAGTGG GGTG 174

(2) INFORMATION FOR SEQ ID NO: 4691:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 363 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4691:

TTTTTTTTTA AAAAAAGGGA AGGGAAAAAnA AAAAGGGAAA AAAATTTAAC CCAAGGGTTT 60
TTAAAGGGGG CCAATTTTTT CCAAAAAAAA AAACCCTTTG GGTAAATTT TTTTAAAAA 120

GTTAAATTTT TTTAAAAAGG GTTCCCTTTT AAATTTTGGG AAAAACCCCC TTTTTTTTTT 240
 TTAAGGGAAT TTAATAAATT TAAGGCCCTC CCCTAAATTA AAATTAAAGG TGGGAAAAAA 300
 5 AAAATTAATT AAAnAACCCA TTTTTTTTTT TTAATTTTTT AACCCAAAGG GGGTAATTTG 360
 GCC 363

(2) INFORMATION FOR SEQ ID NO: 4692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4692:

20 TAGTGTCAAT TTTATTGATA TTTGCAATTA AACTGAAATT TAATTTTTCG GATGTATTTT 60
 nTTTACTTAA AGTAAAATAG AACACGATTT TGATGTCTGG GAATAGTGGA AATGATAAAA 120
 ACTACTAATG ATTGATTAAG TAGTGGTTCT TAACATTAGC CTCAGCTAAT TGTTACTTAA 180
 25 AAATAGGAAT ACATGAGTAA AACTCAnTGG 210

(2) INFORMATION FOR SEQ ID NO: 4693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4693:

ATAGTAGTAA AGTATTTTCT TCCAAACATT TATTTTGATT AAGTCTTCAT CATTAGTATT 60
 40 CTCAGCTCCA CATGCACCAT CTTCCACCTC AACCTATTAA CCTCATCATC TTTAGGATCT 120
 TATAACCAAT TGGAAATCTC ATCTTGAGGn nGCTTCATCT TAGATGCTTT CACACTTATC 180
 CCTCCACACA TAGCTACCCA GCTATCCGT 209

(2) INFORMATION FOR SEQ ID NO: 4694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

GCACATTAAC CnAAGCACCA GGCCATATAG CAATTGTTGA TACAGTATTT AAATATTTAG 60
 CATGTGACGG AATAGTTACA TATGTATTCA CTAAGGCCAT AATGACAAAT CCATTAAAAA 120
 5 GTTGGATGCT TATTCGACCC TGCTAGATGA TCTGATGAAC GGAACGCATA TTAAATAAGT 180
 ACGTGGTTAT GGATCAGTAA GATACTCTAC CAGTTACCAG nG 222

(2) INFORMATION FOR SEQ ID NO: 4695:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4695:

20 TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60
 TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120
 TCTTCAACTA AGTCACGATA TAATGTTTTT GAATTTTCG 159

(2) INFORMATION FOR SEQ ID NO: 4696:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4696:

35 AATATGGTAG TTTTAACTT ATCTATTAAG GTACAATTGA CCAAATCGAT AAAACAAATA 60
 ATACGTATCG TCAGACAATT TATGTCAATC CAAGTGGAGA TAACGTTATT GCGCCGGTTT 120
 40 TAACAGGTAA TTAAAAACCA AATACGGATA GTAnTGCATT A 161

(2) INFORMATION FOR SEQ ID NO: 4697:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4697:

50 CCAAACCTCAA TATGGCTTTA TTGGCACAGG GAACAGATAT GGAAGGTTTT ATTTATGGnT 60

ATATGGGATC AACACACAAA GCCGGACGCA GTGAATATTA CGCAAAATGA

170

(2) INFORMATION FOR SEQ ID NO: 4698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4698:

15	CCACGGCTAA CTACTGCCAG CAGCCGCGTA ATACGTAGTG GCAAGCGTTA TCCGGAATTA	60
	TTGGGCGTAA ACGCGCGTAG GnGTTTTTTTA AGTCTGATGT GAAACCCACG GTCAACCGGA	120
	GGGTCATTGG AAACCTGAAA CTTGAGTCAG AAGAGGAAGT G	161

(2) INFORMATION FOR SEQ ID NO: 4699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4699:

30	TAAATCTTCA TCAATATGAT CTAACCAATA TTGATAAAAC CTTGATGTGT TTCGTGTCAA	60
	TGACATACCA TATCGACTAG GTACCTTTTT AGAATGTTGA TTAATCACAA CAAATATCAT	120
35	GGGCAAGGTC ATCTTGCAAA ATGGATTCTGA TTCAAGTGGG AGGGnCGATG ATGGACGTGC	180
	TGCATGCACT GATGACCCTT TTTGCCCATC CTGGCAAATC CCACCATGAA ATGACTGACG	240
	CGGACGCh	248

(2) INFORMATION FOR SEQ ID NO: 4700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4700:

50	CCCAGCAAG CGAACGTTTG GCACTGTCTC AACGAGAGAC TCGGTGAAAT CATAGTACCT	60
	GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT	120

(2) INFORMATION FOR SEQ ID NO: 4701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4701:

TACAGGGTAG TGAGATTTTCG AAACAATATG GAGAAGCAGG ACTTCCTGGA AAATACAATT 60
 AATGTTTTATA CGAATGGTCA TGCTGGTCAA AGTTCTTGCA GGCATATGCA CCGAAAGCTT 120
 AATGATTCAT CATACTGGAG ATGCCAATGA CTATGTTGGG TAAAGGATTT ATCTGGT 177

(2) INFORMATION FOR SEQ ID NO: 4702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4702:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 60
 GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC AACTGCCGA 120
 GAAAAGnCTC TAGATAGAAA ATAGGTGCCC GTACCG 156

(2) INFORMATION FOR SEQ ID NO: 4703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4703:

CTTGAAAAAG ATGGTTATTC TGTGAAGTA ATTGACTTAC GTACTGTTCA ACCAATCGAT 60
 GTTGACACAA TTGTAGCTTC AGTTGAAAAA ACTGGTCGTG CAGTnGTCAG CAAGACGCAC 120
 AACGTCAAGC TGGTGTGGT GCAGCAGTTG TAGCTGAATT AAGTGA 166

(2) INFORMATION FOR SEQ ID NO: 4704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4704:

GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGnCT CGAACCTACG 60
ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGATTAA TATTATGCCT 120
GGCAACGTTC TACTCTAGCG GAACGTAAGT TCG 153

(2) INFORMATION FOR SEQ ID NO: 4705:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4705:

AGGTAGAGCA CTGTTTGGAC GAGGGGCCCC TCTCGGGTTA CCGAATTCAA ACAAACTCCG 60
AATGCCAATT AATTAACTT GGGAAGTCAG ACACATGGGT GATAAGGTCC GTATTGAAA 120
nGGAAACAGC CCAGACCACC AGCTAAGGTC CCAAATATA TGT 163

(2) INFORMATION FOR SEQ ID NO: 4706:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4706:

TAAGGTTGGG ATTGTTTGTG GGCTCGTTGC CACCCATTGT ACGGCACTCA TCAnTTCAAG 60
CCACCAGCTA CAGTATATCT CCTTGACCAG CCATAATTG ATTGGCTGCA GTCGCGATGG 120
TTTGTAATCC TGATGAGCAG TAGCGATTCA TGTTTGACCh GTACCCGTCA GATATCCGCA 180
GCAATGCAAT GTTGTGCAAG TTT 203

(2) INFORMATION FOR SEQ ID NO: 4707:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4707:

CGGGTGAGAA TCCGTCCACC GATTGACTAA GGTTCCTCAGA GGAGGCTCGT CCGCTCTGGG 60
5 TTAGTCGGGT CCTAAGCTGA GGCGCAGnGT AGGCGATGGA ATAACAGGTT GATATTCCTG 120
TACCACCTAT AATCGTTTTA ATCGATGGGG GGC 153

(2) INFORMATION FOR SEQ ID NO: 4708:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4708:

20 nCTATAATGA ATAAATAATT TAGAAATATG CTTCCGATTG TTCGATGCTT TAATTCAGTT 60
AGAAGCATCA TAGAATGCAT GATTACTGTT GTAAAGATAC GTAATGTTTT GTATTGACTG 120
TATGTCTTTG GATAGAGTTA CAAACTTATT 150

(2) INFORMATION FOR SEQ ID NO: 4709:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4709:

35 AAAATTCTGGG TTCTCAAATC ATCGGAACAT AACAAAACAA CCTAAGCAAC ATGTAGGCCG 60
TTGTCACTTA ACTTCTTGTT TTTCCGATGA CAGCTTCTAT TnAGAGAATG TCATGATTAT 120
40 TTTATATTCA CTTCAATGTT ATCAGTATTA GTGCCA 156

(2) INFORMATION FOR SEQ ID NO: 4710:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 149 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4710:

55 GTTGATATTC CTGTACCACC TATAATCGTT TAATCGATGG GGGGGACGCA TAGGATAGGC 60

TCGTTAAGGC TGAGCTGTGA TGGGGAGAA

149

(2) INFORMATION FOR SEQ ID NO: 4711:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4711:

TTGACTTCAA TACCATGGGC CAGGTACnCT TTAAATGTTG TTGTCTCAGT TAATATTAAT 60
 TGGCTTTTCT TTTGCATAAT TGACAATGGC TTCTGCCAAT GGGTGTTTCAG AATCTTTTTC 120
 AGCAGTAGCA AGTAGTTGGT AGCGTTTGAT TGGTCACCAG 160

(2) INFORMATION FOR SEQ ID NO: 4712:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4712:

ATAGTGAACC AGTACCGTGA GGACnAGGTG AAAAGCACCC CGGAACGACG TGAAATAGAA 60
 CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC GTGCCTTTTG 120
 TAGAATGAAC CGGCGAGTTA CGATTTGATG C 151

(2) INFORMATION FOR SEQ ID NO: 4713:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4713:

ACCAGTTGAT CTACCCTTGG TCAGGTTGAA GTTCAGGTAA CACTGAATGG AGGACCGAAC 60
 CGACTTACGT TGGAAAAGTG AGCGGGATGA ACTGnGGGTA GCGGAGAAAT TCCAATCGAA 120
 CCTGGGAGAT AGCTGGTTCT CTCCG 145

(2) INFORMATION FOR SEQ ID NO: 4714:

- (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4714:

10 TGTnACGCAG AGATCGCGGG TCGATTCCC GTCGAGACCG CCATTTAATT TTATAATTAA 60
 TAGCGATGTA CCTATAATAA TGGAGGAATA CCCAAGTCCG GCTGAAGGGA TCGGTCTTGA 120
 AAACCGACAG GCCTTAACGG GCCGCGGGGG T 151

(2) INFORMATION FOR SEQ ID NO: 4715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4715:

25 TCGTATTGAA TGGCTTCGTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT 60
 GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAAAG TGTAATTTTA CTTTGnAATA 120
 30 CTTTAAAAAA ATAAGACACT TTGCCAACTT G 151

(2) INFORMATION FOR SEQ ID NO: 4716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4716:

40 GCTGTATCG GAAAAACAAG AAGTTAAGTG ACAAGGGTTT ACATGTTGCT TAGCTTCTTT 60
 45 TATTATGCGT AATGATGTAA AAAGACGAAT ATTCATTTGT TTGTAAAAGT GGCATTTCTA 120
 TGTCTTAAAA GTGACGAAAC TTCACnCTGT GC 152

(2) INFORMATION FOR SEQ ID NO: 4717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4717:

GGATACTAGT AAAACCATAT TTAGTAAATA CAGATGGAnT AAATCTTTTA AGGCTTATAA 60
 5 ACGCTCATCT GACATTGTAG AATTCATGCT TTCAAAAGAC GATATACTAC GACACTCCTA 120
 CGAACTTGTC CAAGGATTAC GAAA 144

(2) INFORMATION FOR SEQ ID NO: 4718:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4718:

ATCATAAGGG GCATGATGAT TTACGTCATC CCCACCTTCC TCCGGTTTGT CACCGCAGTC 60
 20 AACTTAGAGT GCCCAACTnA ATGATGGCAA CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA 120
 CTTAACCCAA CATCTCACGA CACGA 145

(2) INFORMATION FOR SEQ ID NO: 4719:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4719:

AAATACCTTT CCACGATCTT CAGCTGGGCG CCTCTGCACT CGCAAACGCA CTTGATGCAT 60
 CAACAACACC ACCAAATAGT CCCTGCAATA ACCTCACAGT ACAAACGTGTA ATGGTGTCGT 120
 40 ACACnATGCC ATTTAAAAAT AGCATACCGG CAAAGC 156

(2) INFORMATION FOR SEQ ID NO: 4720:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4720:

TTAAATCGAG TCTCTTTTAC AGGTCCATAT TTTGTTACGT ATCGACCGGT GGCTAACTAC 60
 55

TAACTCGGAT CAAATTCGTC TCGATGACCT GG

152

(2) INFORMATION FOR SEQ ID NO: 4721:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 146 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4721:

CACTAGTTCA AGTTCAAGTG GCGACGATTG GTATTTTACA AGAATTTTAT CAACAAGGAT 60

TTAATTAGCT TAAACGCnGC AATCCCTGTG TTACTAGGGC GGATAACATT GGTACCACGG 120

TTACAGCTAT CTTAGCTAGT TTAGCC 146

(2) INFORMATION FOR SEQ ID NO: 4722:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 156 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4722:

CCACACCAAT ATTTTGGCGCT AAGTAnATCG CATTAAACGT TTGTCTTCCG CCATTTGAGC 60

CACACTGCTC CAGCTCATAG CGCTATATCG CAGGGAATAA TCATTCCGCC ACCACAACCC 120

TAACATTACC CAGCCATACA GCCATACCAG GGCCAC 156

(2) INFORMATION FOR SEQ ID NO: 4723:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4723:

ACGGTCTTGC TGTCATTAT AGATGGATCC GCGCTGCATT AGCTAGTTGG TAAGGTAACn 60

GCTTACCAAG GCAACGATGG CATGAGCCGA CCTGGAGAGG GTGGATCGGG CCACACTGGG 120

AACTGAGACA CGGTCCAGAC TCCTACGGGG AGGCAGCAGT A 161

(2) INFORMATION FOR SEQ ID NO: 4724:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4724:

10 CAGAAAGCTC ACGGGGCTTT CGTCTGTCGC GGGTAACCTG CATCTTCACA GGTACTATGA 60
 TTTCACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGnCTTTCGT GCGGGTCGGA 120
 ACTTACCCGA CAAGTAATTT CGCTACCTTA GGACCGTTAT AGTTA 165

15 (2) INFORMATION FOR SEQ ID NO: 4725:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4725:

GGACGTTATA AGTGCTGAAA CATCTAAGCA TGAAGCCCC CTCAAGATGA nATTTCCCAA 60
 CTTTCGGTTAT AAGATCCCTC AAAGATGATT AGGTTAATAG GTTCGAGGTG GAAGCATGGT 120
 GACATGTGGA GCTGGACGAA TACTAATCG 149

30

(2) INFORMATION FOR SEQ ID NO: 4726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4726:

TTGAATTTTT GAAAAAATA TGCCGAAATA AAAGATGCCA AGATATCCGC CGGGTAAAAA 60
 ATTAAGTTTC CGAAAAACCA GGTGTTGGTA CCCATTGCAT CTGGGGTGGC AAAAGCATTT 120
 GCAGATAAAA TTGTCATCAG TGGTTACGAT GGTGGTACAG GGCTTCACCC AAACGAGTAT 180
 CAGCATGCCG GTGTTCTTGG GAGATGGTTA GCAGAACACA TCAACATAAA CTAATGCTAA 240
 GAnCGGTAAA GTAGACAnCG GTAGTATACT GAAAT 275

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(2) INFORMATION FOR SEQ ID NO: 4727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4727:

ATCAATGAAC AACACATACA GATGGTACTG CGACGCCTAG AGTAACAAAA TAAGTTTTGT 60
AACTCTATCC AAAGACATAC AGTCAATACA AAACATTACG TATCTTTACA ACAGTAATCA 120
TGCATTCTAT GATGCTTCTA ACTGAATnA 149

(2) INFORMATION FOR SEQ ID NO: 4728:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4728:

GCACGTTATT CCATTATCTT AATGGTTATC TTATCCTCAA CTAAATTGGA GGAATCACTA 60
TGACAATTAA TAAAGAACCG TTCTTGGCGC AGCACAATGG GCGCTCACTG GCAGACTTTT 120
GTGATGCTGA CTAAAGTAA ACTATTAGAT ATTGnGTG 158

30

(2) INFORMATION FOR SEQ ID NO: 4729:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4729:

TCATTGACAT CGCTGGAATA GGTGTAAATC CTGCGATTCTG ATCTGGACCA TATTTTTTTTA 60
TTGTATACAG TAATTGTGCT GCGATTATCT CTGTAACGTC TTTCCAATTT GAnCGCACGT 120
GCCCTCCCAT ACCTCGGG 138

45

(2) INFORMATION FOR SEQ ID NO: 4730:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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TAAAGACTAT ACCATTCTAT CCAATAATAA TTGGATTCCG ATTTGTCTGA ATTCGTAACC 60
 GAGAGGCCCC TCGTCCAAAC AGTGCTCTAn CTCCAATAAT CATCACTTGA GGCTAGCCCT 120
 5 AAAGTATTTT GGAGAGAACC AGCTATTTCC AGTTCGATTG GAATTTCTCC GCTACCCTCA 180
 GTTCATC 187

(2) INFORMATION FOR SEQ ID NO: 4731:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4731:

CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT TCGCCATTAA AGCGGTACGA 60
 AGCTGGGTTC AGAACGTCGT GAGACAGTTC GGTTCCCTAT CCGTCGTGGG CGTAGGAAAT 120
 TTAAGAGGAG CTGTCCT 137

(2) INFORMATION FOR SEQ ID NO: 4732:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4732:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60
 TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120
 40 TCTTCAACTA AGTCACG 137

(2) INFORMATION FOR SEQ ID NO: 4733:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4733:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60

TCTTCAACTA AGTCACG

137

(2) INFORMATION FOR SEQ ID NO: 4734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4734:

AAAACATAAA TACAAAAATA TAGCTATTAC TATAAAAAAC AGCAGTAAGC ATATTTCCAA 60
 ATTGCAAATT ATCCTACTGC TGTTCTTTTT GGGCAGTGGG nACAGCAAAT GATATTTTCG 120
 ACAAATTTTA TTTCGTCGTC CCACCCCAAC TTG 153

(2) INFORMATION FOR SEQ ID NO: 4735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4735:

TAGAAATTAC GGACCCAATT TCTCTATGTT GGGGCCCATC CCCAACTTGC ACATnATTGC 60
 AAGCTGACTT TTCGTCACCT GCTTTGTTGG GGCCCCGCCA ATAAGCGTTG TAGTGCCTAG 120
 TACTTTGATT GATGTCCAAG TT 142

(2) INFORMATION FOR SEQ ID NO: 4736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4736:

ATGTTATTCA AAGTAAATTG CTTTGCCTGA TTTTGCAGAC TGATAAATCG CTTCAAGAAT 60
 TTTTGTAACCT ACCATTGCTT GTTCCGGTTT CACAACTGGT TCAGTATCAT TTACAACnGC 120
 ATCAATCCAA GCTTTTG 137

(2) INFORMATION FOR SEQ ID NO: 4737:

- (A) LENGTH: 144 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4737:

10 GGTCGTTTAG TATTTGGTCG TACACGCAA ACCAGGTGCA TCTACCCTTG GTCAGGTTGA 60
AGTTCAGGTA AACTGAAAT GGAGGACCGA ACCGACTTAC GTTGAAAAT GAGCGGATGA 120
ACTGAGGGTA GCGGAGAAAT TCCA 144

15 (2) INFORMATION FOR SEQ ID NO: 4738:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4738:

25 GGGTAGCTAT GTGTGGACGG GATAAGTGCT GAAACATCTA AGCATGAACC CCCCTCAAGA 60
TGAGATTTCC CACTTCGGTT ATAAGATCCT CAAAGATGAT GAGGTTAATA GGTGAGGTTG 120
30 GAACATGGTG ACATGTnATC TGCTTTTCTA ATCATAC 157

(2) INFORMATION FOR SEQ ID NO: 4739:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4739:

40 GCTTTATGTC TAAACGTCA AAATAAAAAG CAAACACAAA GAAAAATGGC TTGGCGAAGT 60
GAAAACGGTT GAATCTGACG AAACGAGAAA AGAACGCAAC GAGTTTAGTA GAGCTAnATG 120
45 AGTAAGTGAG AGCCGAAGAG AGGGA 145

(2) INFORMATION FOR SEQ ID NO: 4740:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 234 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4740:

5	TAGTAGCACC ACCCTTAGAC CTTCTTGATT TGACATCGTT GTTCTTCCTT CCTTCGGTCT	60
	CGTTACTCAT TTAGCTCTAC TAAACTCGTT GCGTCTTTTC TCGTTTCGTC AGATCAAACG	120
	TTTCACTTCG CCAAGCCATT TTTCTTGTGT TTATTTTATT TGACGTTTAG ACATAAAAAA	180
10	GAGACCCACG TTCAACTTGC CnGCACGTTT TACTCTGCGG AnTAGTGGCT ACCA	234

(2) INFORMATION FOR SEQ ID NO: 4741:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 135 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4741:

20	GCAAGTCTTT TTAAAGGTAA CACTATCATT TATGCAATAC GGCGCATTAC CAGAGTTGCA	60
	TGGTCAAAAT ATATTGTTGT CATTGAAGA TGGACGTGTA CAAAATGCG TGTTACGTGA	120
25	TCATGATACT GTCAn	135

(2) INFORMATION FOR SEQ ID NO: 4742:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 145 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4742:

35	ACCCTGGTAC AGTTGAATTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA	60
40	AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGA GAnAGCTGGT	120
	TCTCTCCGAA ATAGCTTTAG GGCTA	145

(2) INFORMATION FOR SEQ ID NO: 4743:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4743:

TGATTATCAT GGGTGC GGGT ATTAACCATT GGTTTAACTC AGATACGATT TATnGTGCAA 120
 TCTTAAACTT AGTTATGGTA TGTGGCGTCA A 151

(2) INFORMATION FOR SEQ ID NO: 4744:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4744:

TAAAGCTAAA AACACAGCTC ATAATATCAA AAAAGGTGCA GAAGAAATGG TTGAAGCGGC 60
 AGGCGATAAA ATCAnAGATG GTGCATCTTG GTTAGGCGAT AAAATCGGCG ATGTGTGGGA 120
 TTATGTACAA CA 132

(2) INFORMATION FOR SEQ ID NO: 4745:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4745:

CGTGCCTCT AACCAGCTGA GCTATAGGCC CATTAAATTG AATGAACAAA CATTCAAAAC 60
 TGAATACAAT ATGTCACGTT ATTCCGCATC TTCTGAAGAA GATGTTCCGn ATATATCCTT 120
 AGAAAGGAGG TG 132

(2) INFORMATION FOR SEQ ID NO: 4746:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4746:

GTGATCCGAC TCAGATAGCG ATCCGACTCA GATAGCGACT CAGATTCAGA CAGCGATTCA 60
 GATTCAGACA GCGATTCAGA TTCAGATAGC GATTCAGATT CCGACAGTGA CTCAGATTCC 120
 GACAnTGACT CGGATTCA 138

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4747:

CATTATTGTA AACTGAACTT TTCGTCACCT GCTGGTGTGTT GGGGACCCCA CCAACTTGGC 60
 ACATTATTGG TAAGCTGACT TTTCGTCACCT TACTGTGTTG GGGCCCCGCC AACTTGCACT 120
 GTCTGTAGAA ATTGGGAATC CAATTCTCT ATGTTGGGGC CCACACCCCA ACTCGACATT 180
 GCCTG 185

(2) INFORMATION FOR SEQ ID NO: 4748:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4748:

ACCGAATCCC TTCAGACCGG TACTTGGGTA TTCCTCCAAA ATTATATGGA CCTTGACAGT 60
 ACTCGAACCT GACGTACCGA AACGGTTATG AAGACCGTTA nCTCTAACCA ACTGAGCTAA 120
 AGGATCCTAA ATATAATTTT ACAACTAATA AATAGTGGAC GGTGGAGGGA TCG 173

(2) INFORMATION FOR SEQ ID NO: 4749:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4749:

ACACAAGGAT AAGGCATTGT TGGATGTGGG ATGCTTTAAC TGGGCAAGCG ATTGGTCGTC 60
 CTAAAACAGG TACATATGCC GGCTATCTGA CCTAGTCGGT TTAGATATTG CAGTGTCTGT 120
 AATTAAAGGG CATGCAACCA AGTAnCTGAG GAAACAACTT ATTTTCATGG TGTCAAAAAT 180
 TGnTAAATAC GGTGTTTGAC AATTGCGCAC CT 212

(2) INFORMATION FOR SEQ ID NO: 4750:

- (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4750:

10 AATCTCAGGT TTTACCAAGC AAAACCGATG AATAAAGAGT TTAAATAAG CTTGAATTCA 60
 TAAGAAATAA TCGCTAGTGT TCGAAAGACn GCAGCAAGAT TAATAACGCG TTAAATCTT 120
 TTTATAAAAAG AAAACGTTTA 140

15

(2) INFORMATION FOR SEQ ID NO: 4751:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4751:

25 ATTGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT CATCATCTTT 60
 GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGTTCAT GCTAGATGCT 120
 30 TCAGACTATC CCGTCCACAC ATGTAACCAG nATGCGTGGA CGCATGGAAC AGGGATGTCA 180
 TCCG 184

(2) INFORMATION FOR SEQ ID NO: 4752:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4752:

45 GGGATCTTCC GCAATGGGCG AACTGTACG GAGCAACGCC GCGTGAGTGA TGAAGGTCTT 60
 CGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACTGTG CACATCTTnA 120
 CCGTACCTAA TCA 133

50

(2) INFORMATION FOR SEQ ID NO: 4753:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4753:

5 GTATGCTGTG TGGCTTGTCA TGTTCTGGGTT TGGTGGCGGA CCTGATTATT CCTGCGnTAT 60
ACGCTATGGC TGGAGCAGTG TGGCCAAATG GCGGAAGACA AACGTTTAAT GCGATCTACT 120
TGGCGCAAAA TATTGGTGTG GCTGTCTGGTG CTGCAATGGG CG 162

10 (2) INFORMATION FOR SEQ ID NO: 4754:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 134 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4754:

20 AATTCGATTC CCTTAGTAGC GCGGACGAAA ACGGGAAnGA GCCCAAACCA ACAAGCTTGC 60
TTTGGGGGTT TGTAAGACAC TCTATACGGG GTTAACAAAG GACGACATTA GACGAATCAT 120
25 CTTGGGAAAG ATGA 134

(2) INFORMATION FOR SEQ ID NO: 4755:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
30 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4755:

AGAGTGCCTA ATAGCTCACT AGTCGAGTGA CACTGCGCCG AAAATGTACC GGGGCTAAAC 60
40 ATATTACCGC AAGCTGTGGA TTGTCCTTTG GACATGGCTA GGAGAGCGTT CTAAGGGCGT 120
TGAAGCATGn ATCGTAAGG 139

(2) INFORMATION FOR SEQ ID NO: 4756:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4756:

CGTGAAATGC GCAGAGATAT GGAGGAACAC CAGTGGCCGA AAGCCACTTT CTGGTCTGTA 120
 ACTGGACGCT GGATGTGCCA AACCTGGGGG ATCAAACAGG TTA 163

(2) INFORMATION FOR SEQ ID NO: 4757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4757:

CATGAACTA GATAAGTAGT AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG 60
 TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ATCACAGAT 120
 TAATACCGCG TTTAATCTTT TATAAAGGAC CGTAACTTCA 160

(2) INFORMATION FOR SEQ ID NO: 4758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4758:

TACATGGGTT TATTGTTGAA GATGACGAAA TTGTAGAAAT TTAATATTCT AAAAAGGTTG 60
 GGGACATAAA TCCCCCTAAA AAAACCAGCA GTAAGATAAT TTTCAATTAG AAAATATCTT 120
 ACTGCTGTTC TCTATTTATA CCAATTACT TTCGTAATTG TTAAAATTTT AAAAGGA 177

(2) INFORMATION FOR SEQ ID NO: 4759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4759:

CGGTGTGTAC AAGACCCGGG AACGTATTCA CCGTAGCATG CTGATCTACG ATTACTAGCG 60
 ATTCCAGCTT CATGTAGTCG AGTTACAGAC TACAATCCGA ACTGAGAACA ACATTATGGG 120
 ATTTGCT 127

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4760:

GGGCCCCTCG TCGGGTTACC GAATTCAGAC AAACCTCCGnA ATGCCAATTA ATTTAACTTG 60
GGAGTCAGAA CATGGGTGAT AAGTCCGTGT TCGAAAGGAA ACAGCCCAGA CCACCAGCTA 120
AGTCCCAAAT ATATGTTAAT GAAAG 145

(2) INFORMATION FOR SEQ ID NO: 4761:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 228 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4761:

TAAACAAGGC GCGTTGGGCC TATTCAGTGC GGCTCTTCTG GCGGTTAACC CTAAAGAGCA 60
CCCCTTCTCC CGAAGTTACG GGGTCATTTT GCCGAGTTCC TTAACGAGAT TGCTCGCTCA 120
CCTTAGAATT CCATCTGACT ACGGTCGTTG CGTACGGCAC TATTTCTTCA AGCTTCCGCA 180
TTAACACACC AAAACAGCTC CCACCACCAC TAAATCGAnC AACACTAG 228

(2) INFORMATION FOR SEQ ID NO: 4762:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4762:

TnGCCAAATC TTAGTAGTCG CTTGGTTCGG TTGTGGTGCG ACAGCTGTGA AATCATCACT 60
ACGTTGCTCA TCACTCACTG TCTCTCCGCT TCCTTGCCTT GCAACAGCTT GAATTGTATC 120
AGCAGGGTTG 130

(2) INFORMATION FOR SEQ ID NO: 4763:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4763:

CAACTCGTAG TCAGGGTCGA AAGACGGGAC TTAGTGATCC GGTGGTTCCG TCATGGGTAG 60
GGCCATCGTC TCAACGGTAT AAAAGCTACC CCGGGGATAA CAGGCTTATC TnCCCCAAGA 120
GTTACATCG ACGGGGAGGT TTGGCACCTC G 151

(2) INFORMATION FOR SEQ ID NO: 4764:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4764:

ACCCCAACTT GCATTGnCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCCGC 60
CGGCAAGGTT GACTAGAATT GACCAAAAGC TTGTTACAAG CGCATTTTCG TTCAGTCAAC 120
TACTGCCA 128

(2) INFORMATION FOR SEQ ID NO: 4765:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4765:

AATACAGCCC CAGAGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT CGATGTGAAC 60
TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG CGGATGGCCC 120
TTTCCATGTG GnAAC 135

45

(2) INFORMATION FOR SEQ ID NO: 4766:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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GATTCTCACC CGTCTTTTCG CACTCACACC GGCATTCTCA CTTCTAAGCG CTCCACATGT 60
 CTTACGATC ATGCTTCAAC GCCCTTAGAA CnCTCTCCTA CCATTGTCCA AAGGACAATC 120
 5 CACAGC 126

(2) INFORMATION FOR SEQ ID NO: 4767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4767:

TTAATAGTTT TATAAGAGAG GTGTTTGATC TTGAGCTAAC CACnTCATTC GAGTACTGTC 60
 20 ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT GGGGTATATG CATATAAGAT 120
 GATTTTTTAAC 130

(2) INFORMATION FOR SEQ ID NO: 4768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4768:

GTTAACCCTA AAGAGCACCC CTTATACCGA AGTTACGGGG TCATTTTGCC GAGTTCCTTA 60
 35 AnGCGCGTTC GATCGCTCAC CTTAGGAATT CTCATCTTGA CTACCTGTGT CGGTTTGCGG 120
 TAGGGCACCT ATTTTCCTAT CT 142

(2) INFORMATION FOR SEQ ID NO: 4769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4769:

CCTTGGGACC GACTACAGCC CCAGGATGCG ATGAGCCGAC ATCGAGGTGC CAAACCTCCC 60
 50 CGTCGATGTG AACTCTTGnG TGGAGATAAG CCTGTTATCC CCGGGGTGAG CTTTGTATCC 120

(2) INFORMATION FOR SEQ ID NO: 4770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4770:

CTAAAAGTTG TATTTTAAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA 60
ACCGTTAAAC AATGCATAGT TTGCTTAACT TCCAATATTG ACTCATCATT ACAATTGACA 120
TAGAGCTATT AAGCGTnGCC ATGAG 145

(2) INFORMATION FOR SEQ ID NO: 4771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4771:

TCGAGTGACA CTGTCGCCGA AAATGTACCG GGGCTAAACA TATTACCGAA GCTGTGGATT 60
GTGCCTTTGG AAATGGTGAG GnGAGCGTTC TAAGGGCGTT GGAAGCATGA TCGTAAGGAC 120
ATGTGGGA 128

(2) INFORMATION FOR SEQ ID NO: 4772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4772:

GGGCAGATGT TCCTGCAGTC ATAGTGCCGT CAACTTTAAA TACTGTACGT AATTTGGCTA 60
ATGCCTCCAT CGTGGnTGTC AGGGCGTATA AATTCATCTT GGGTCAAAGA TATTTGGTGT 120
GTACTT 126

(2) INFORMATION FOR SEQ ID NO: 4773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4773:

GTCTTTTCTC GTTTCGTTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT 60
GTTTACTTTT TATTTTGACG TTTTAGGATA AAAAAAAGAn ACCTTGCGGT CTCAATGCGG 120
CTCATC 126

(2) INFORMATION FOR SEQ ID NO: 4774:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4774:

ATTTCAATAT CAGGCTACAG TAAAGCTCCA CGGGGTCTTT CCGTCCTGTC GCGGGTAACC 60
TGCATCTTnA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 120
TACG 124

30

(2) INFORMATION FOR SEQ ID NO: 4775:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4775:

ACCAAGTGAG CCGGAAACAC CAACGCCACC AACACCAGAA GTACCAAGTG AGCCGGAAAC 60
ACCAACACCA CCGACACCAG AAGTGCCGAG TGAnCCAGAA ACTCCAACAC CGCCAACACC 120
AGAG 124

45

(2) INFORMATION FOR SEQ ID NO: 4776:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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CCCGCTAGTC TCCACCATT TTTTTTTACA CGATGAACAT TGAAAACThA ATACAATATG 60
 CAACGTTAAT TCCAAAAAAC GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT 120
 5 AATCAAACAT CATAA 135

(2) INFORMATION FOR SEQ ID NO: 4777:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4777:

AGTGCAGAAG AGGAAAGTGG AATAnCCCCA ACATAGCGGT GAAATGCGCA GAGATATGGA 60
 20 GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAAC TG GACGCTGGAT GTGCGAAACG 120
 TTGGGGGTTC AAACAGGATT TAGA 144

(2) INFORMATION FOR SEQ ID NO: 4778:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4778:

AATTTTGTGAT GACGGGTCCC TTCCTAGGGT GCCGTCTCAG CCACCCCAAC CGGCACATTG 60
 35 TTGTAAGCTG ACTATATGTC nTTCATGTGT TGGGGCCCCCT GTCTTCGACT GGCACTGCTC 120
 CCT 123

(2) INFORMATION FOR SEQ ID NO: 4779:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4779:

GCGCATTAAC TATCGCGATA TTAATCGCTA TTCTATATCG TCACTTTAGA GGATATCCTG 60
 AACAAATATAG CTCAGGTATT ACGTTTTCAT CTAAATATTT ATTAAGATTT GCAATCATCC 120

(2) INFORMATION FOR SEQ ID NO: 4780:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4780:

GGTAATATGT TTAGCCCCGG TACATTTTCG GCGCAnTGTC CTCGACTAGT GAGCTATTAC 60
 GCACTCTTTA AATGATGGCT GCTTCTAAGC CAACATCCTA GTTGTCTGGG CAACGTCACA 120
 TCCTTTT 127

(2) INFORMATION FOR SEQ ID NO: 4781:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4781:

ACACnGGGTG AGAATTTGTC GCTATTTGTA AATTGTATCC TGGCTTAAGT TGGCCAAAGT 60
 GTCTTATTTT TTAAAGTAT TTTAAAGTAA AATTACATGT TAATACGTAG TATTAAATGG 120
 CGAGACTCC 129

(2) INFORMATION FOR SEQ ID NO: 4782:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4782:

CTCATTCCCG TTGCATTTTA TCTTCTGCAA CAACAACATT TCGTCTTTAT CGTCTTCCAT 60
 AGTAGTAGGA TTTTCTACTA CTTGACCATT CATAATCTGT TGCATTTTCAT GTTTGnTTTG 120
 GTCAGATTTA GGACCA 136

(2) INFORMATION FOR SEQ ID NO: 4783:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4783:

CATCAACATC GGCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 60

10 AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGATT ATTGnGACGG TATTGTTGG 119

(2) INFORMATION FOR SEQ ID NO: 4784:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4784:

ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC ATACGTGTTT TAACCTGCGT 60

25 nATCCCATTG CATCCATAA TTGTGAATGG ACCAAGTTTC CAGTTGAACC CCCAGACAAG 120

CGCACGG 127

(2) INFORMATION FOR SEQ ID NO: 4785:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4785:

ACACCGGCAT GCTGAATACT CGTTTTGGGT GAAGCCCCTG nACCACCATC GTAACCACTG 60

40 ATGACAATTT TATCTGCAAA TGCTTTTGCC ACCCCAGATG CAATGGTACC AACACCTGT 119

(2) INFORMATION FOR SEQ ID NO: 4786:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4786:

CTTTCTAAAC CCGnCAACCAC TTTATCGTGG TGGGGAGACA GTGTTTCAGGC GGGCCAGTTT 60

55

AATCATTTCAT AGAGTGT

137

(2) INFORMATION FOR SEQ ID NO: 4787:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4787:

GTTTTAAACA CTGTTACCGT TTTCATCTTT TAATGTTACC GTTACGCCAG AnATACCTTT 60
TTCATCTTGG TCTTGGATAC CATTITTATT TGTATCTTCC CAGACATAGT CACCTAAGT 119

(2) INFORMATION FOR SEQ ID NO: 4788:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4788:

CATGCTTCCA CCTCGAACCT ATTAACCTn C ATCATCTTTG AGGGATCTTA TAACCGCAGT 60
TGGGAAATCT CATCTTGTAG GGGGGCTTCA TGCTTCAGAT GCTTTGCAGC ACTTAGCCCCG 120
GCCACACATA GCTACCCAGC T 141

(2) INFORMATION FOR SEQ ID NO: 4789:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4789:

CTGGGTTTCAG AACGTCTAAG CAGTTCGGTC CCTATCCGTC GTGGGCGTAA GAAATTTGAG 60
AGGAGCTGTC CTTAGTACGA GAAGACCGGG ATGGACTACC TCTnGTGTAC CAATTGTCGT 120
GCCAACGCAT AGCTGGGTA 139

(2) INFORMATION FOR SEQ ID NO: 4790:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4790:

CATTATTTAG TATTTATGAG CTAATCAAAC AnCATAATTT TTATGGAGAG TTTGATCCTG 60
GCTCAGGATG AGCGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGACGAGATG 120
CTTGCTTCG 129

(2) INFORMATION FOR SEQ ID NO: 4791:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4791:

GGGTGCTCTT TAGGGTTAAC GCCCAGAAGA GCCGCAGTGC AATAGGCCCA AGCGACTGTT 60
TATCAAAAnC ACAGGTCTCT GCTAAACCGT AAGGTGATGT ATAGGGGCTG ACGGCTTCCC 120

(2) INFORMATION FOR SEQ ID NO: 4792:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4792:

CAAATTCTTT CGCTACTTGA ATGACAACAC TTTGTTTTAC GCCTGAAATG GCTTCTTGCC 60
AAGCAGGTGT ATATTTTGAT TCTGCATCGT CGTATCCTTT TGATCTAATT ATGATCAAAC 120
CGn 123

45

(2) INFORMATION FOR SEQ ID NO: 4793:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4793:

AGTTTTGAAT GTTTGTTCAT TCAAATTAAT GGGCCTATAG CTCAGCTGGT TAGAGCGCAC 120
nCCTGATAAC 130

5 (2) INFORMATION FOR SEQ ID NO: 4794:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4794:

CACAGCCACA AGTGATTAAA GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT 60
TAACTCATTT TTCAATAGAT CAGGAAGACT ACCAAGCTTA TGTnGAAGGA CATCT 115

20 (2) INFORMATION FOR SEQ ID NO: 4795:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4795:

nTTAAAAAAA ATTCCCAATT TTTTnTGGGG GGTnGGGAAT TTAAAAATTT GGTTTTTAAC 60
CCAAAGGCC CTTTCCCAA AATTnTAATT CCCTTAAAA TTAAAAATTT GGGAATTTTT 120
TTTnGGCCC AAAATTTTTT CCCTTTTTTT AAAGGCCCA ATTTTTTAATT TAACCCTTAA 180
AACCCCAAA CCTTTTTTCC TTTTTTAAAA TTTTTTTAAA TGGA 224

40 (2) INFORMATION FOR SEQ ID NO: 4796:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4796:

TCGCGTACCG CTTTAATGGG CGAACAGCAA GACCTTGGGC ACCGACTACA GCCCCAnGAT 60
GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCnTCGAT GTGAACTCTT GGGGGCAGAT 120

55 (2) INFORMATION FOR SEQ ID NO: 4797:

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4797:

10 AATTCGATTC CCTTAGTAGC GGCGAGCGAA ACGTGAAGAG CCCCA_nACCA ACAAGCTTGG 60
 CTGTTGTGGT TGTAGGACAC TCTATAACGG GAGTTACAAA GGACCGACAT TAGACGAATC 120
 ATCTG 125

15 (2) INFORMATION FOR SEQ ID NO: 4798:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4798:

CAAAATAATG ACTCCTACGG G_nCTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 60
 AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACC 113

30 (2) INFORMATION FOR SEQ ID NO: 4799:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4799:

CCGGTGGGAG GTAACCTTTT AGGAGCTAGC CGTCG_nAGGT GGGACAAATG ATTGGGGTGA 60
 AGTCGTAACA AGGTAGCCGT ATCGGAAGGT GCGGCTGGAT CACCTCCTTT CTAAGG 116

45 (2) INFORMATION FOR SEQ ID NO: 4800:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4800:

TCAGTGCAT GATTTCGTGAA ATTGAAACGC AAGATTTCGA TATCGAnCAC CT

112

(2) INFORMATION FOR SEQ ID NO: 4801:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4801:

ATAGGATAGG CGACGTGCGA TTGGATTGCA CGTCTAAGCA nTAAGGCTGA GTATTAGGAA 60
 ATCCGGTACT CGTTAAGGCT GACTGTGATG GGGAGAAACA TTGTGTCTTC 110

(2) INFORMATION FOR SEQ ID NO: 4802:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4802:

GAACCAAGTT GTTATTGAAA AnTCGTTTCGT AAAGTTACGG TACGCCCACC GTGAGTGCTT 60
 TTACTIONCTAT ATCAGCACCT ACTGTATCTT TCATTAATTT AACGTCTTCT GCAGTCGCAC 120
 CGCCACCTGC AAAACCTGTT GAATTTTACG AGTCCGCACC GCGCTTTGTA ATCATnCTTA 180
 CATTCTCTGT CACAACGCCA TACCTTCGGG ACTGACTCAC AGCTCAGCGG AACACAA 237

(2) INFORMATION FOR SEQ ID NO: 4803:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4803:

CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA CCAATTGAGC TAAGCCGGGC 60
 AATATGTAAG AATAAATGGT GGAGAATTGA CGGGTTCGAA CCGCCGAnCC TCTG 114

(2) INFORMATION FOR SEQ ID NO: 4804:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4804:

GGATCAAACA GGATTAGATA CCCTGGnTAG TCCACGCCGT TAAACGCATG AGTGCTAAGT 60
GTTAGGGGTT TCCGCCCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCT 113

(2) INFORMATION FOR SEQ ID NO: 4805:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4805:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC GCATCAGCGT CnGTTACAGA 60
CCAGGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT CTGCGCAT 108

25

(2) INFORMATION FOR SEQ ID NO: 4806:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4806:

TTTCAGCACT TATCCCGTCC ACACATAGTC TACCCAGGCT ATGCCGTTGG CACGACAACT 60
GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGAnAGCTC CTCTC 115

40

(2) INFORMATION FOR SEQ ID NO: 4807:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4807:

CAGCCACATA ACATAACTAA GTTTAAGATT GAACGATAAA TCGTATCTGA GTTAAACCAA 60
TGGTTAATAC CCGCACCCAT GATAATCATT GAACGCCTTC AGTATCGTAG GTTTGGAATT 120

55

(2) INFORMATION FOR SEQ ID NO: 4808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4808:

TGCTTACATC ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGCAGCTAA ATTACCTTGC 60
ATCATTGCTA GCTTTTCTTG TATTAAGTGA TATTACTAA TTGGTTTGCC GAATTGCT 118

(2) INFORMATION FOR SEQ ID NO: 4809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809:

TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTCTGA TTGGAATTTTC 60
TCCnATACCT CAGTTCATCC GCTCACTTTC AACGTAAGTC GGTTCGGTCC TCATCAGTGG 120
TACCTGACTT CAACTGACCA GGGTAGACAC 150

(2) INFORMATION FOR SEQ ID NO: 4810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:

AAGAAGGCCGA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCA 60
AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA 107

(2) INFORMATION FOR SEQ ID NO: 4811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4811:

AGAGTGnATT AGGTTATGAA GGTGGGCAAA ATAGGGTAAC CAGTCATTCG AGGAAGACAC 60
 5 AGAAGAAGAC AAACCTAAAT ATGAACCAAG GTGGCATATC GTAGATATCG ATTTCCA 117

(2) INFORMATION FOR SEQ ID NO: 4812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4812:

CTTTTATCCG TTGAACGATG GCCCTTCCAT GCGGAACCAC CCGATnACTA AATCCGTCTT 60
 20 TCGACCCTGC TCGACTTGTA AGTCTCGCAA TCAAGTCCCT TATGCCTTTA CACTCTATGA 120
 ATG 123

(2) INFORMATION FOR SEQ ID NO: 4813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4813:

TAACCCGAGA GGGTCCCCTn GTCCAAACAG TGCTCTACCT CCAATATCAT CACTTGAGGC 60
 35 TAGCCCTAAA GCTATTTTCGG AGAGAACCCAG CTATCTCCAG GTTCGA 106

(2) INFORMATION FOR SEQ ID NO: 4814:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4814:

CTATTGCTTT AGATGCATAT GAATCATTGA nTGACGCGAT GCCGATGATT TCTGAACACG 60
 50 GAATCGCGAA CGTTGGCCAA CTGCCAACGA TTGGCGTGGG AATCATCCAG TG 112

(2) INFORMATION FOR SEQ ID NO: 4815:

- (A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4815:

10 ACGTGGAGAG CATGTCCGTT CAAGCAGAGG GCGGCGGTT GAACCCGTCA TTCTGCACCA 60
TTTATTCTTA CATATTGCCG GACTAGCTCA ATTGGTAGAG CAACTGACCT TGTAATCAGT 120
AGGTT 125

15

(2) INFORMATION FOR SEQ ID NO: 4816:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4816:

GTGCTGGCGC AGTTGCGATG GTTATTGCAC ATAATCCAAG CATGGCATT AATGAAGATG 60
CTGTTGCTTA CACTGAAGAC GTTTATGTT TCTGGCGTCC AACT 104

30

(2) INFORMATION FOR SEQ ID NO: 4817:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4817:

GTCGGGTAAG TTCCGGCCCG CACGAAAGGC GTAACGATTT GGGCACTGTC TCAACGnGAG 60
ACTCGGTGAA ATCATAGTAC CTGTGAAGAT GCAGGTTACC CGCGGCAGGG CGGAAAG 117

45

(2) INFORMATION FOR SEQ ID NO: 4818:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4818:

TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGACGCTCT TTTCTCGnTT CGTCAGATTC 120

A 121

(2) INFORMATION FOR SEQ ID NO: 4819:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4819:

TCAGTTCGGT ATTGTGAGTC TGCAACTCGA CTGACATGAA GCTGGAATCG CTAGTAATCG 60

TAGATCAGCA TGCTACGGTG AATACGTTCC CGGGTCTTGT ACACAACGCC CGTnAAGA 118

(2) INFORMATION FOR SEQ ID NO: 4820:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4820:

CAAACAGTGC TCTACCTACA ATAATCATCA CTTGAGGCTA GCCCTAAAGC TATTTTCGGAG 60

AGAACCAGCT ATCTnCAGGT TCGATTGGAA TTTCTCCGCT ACCC 104

(2) INFORMATION FOR SEQ ID NO: 4821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4821:

TCGTAGTGGT TTCCAACCAA GTTTTTATAA GTCAAACGCT CACATACGGC TTCGTTTTCA 60

TTATTTTAAA TGCTCATTTA CATAGTnAAC TCGCTTTAAA ATAATTTAAC TCATGTCGCT 120

AACGTTTTTCT TTTATAAAAG TTAAACGGTT TTATCTGTGG TGTCT 165

(2) INFORMATION FOR SEQ ID NO: 4822:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4822:

GAGTTTGATC CGGGCTCAGG ATGAACGCTG GCGGCGTGCC TAATACATGG CAATCGAGCG 60

10 AACGGACGAG AAGCTTGCTT CnCTGAGGTA GCGGCGGACG GGTGAGTAAC ACG 113

(2) INFORMATION FOR SEQ ID NO: 4823:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4823:

CCGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCTACC ATCGACGCTA AGAACCTTTC 60

25 TTTGAnTTGT GACAATCGCT TGCTTCTTTC CTCTTCTTCG GCTCTC 106

(2) INFORMATION FOR SEQ ID NO: 4824:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4824:

TAAACGGCGG CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCTTGTC GGGTAAGTTC 60

40 CGACCCGCAC GAAAGGCGTA ACGATTGGG CACTGTCTCA ACTAGAGn 108

(2) INFORMATION FOR SEQ ID NO: 4825:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4825:

TCTAGTGACC GATAGTGAAC CAGTACCGTG AGGATAAGGT GAAAAGCACC CCGGAAGTAG 60

55 nTGTAATAG AACCTGAAAC CGTGTGCTTA CAAGTAGTCA GAGCCCGGTA ATGGGT 116

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4826:

ATAATATTGT AAATTAATCC ATTGATGCCA CAAGTGCCGG ACCAGAAATG ATGGTATTTA 60
ATAATGTGCC ATCTTTATCT TTACGCCAAT CATAATTGGT AAAAATTCCC CCTTCTAATA 120
ATCCTTGTAT TGCCTGTCAT AaAGTCTTTG CTCCTTGAC 160

(2) INFORMATION FOR SEQ ID NO: 4827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4827:

CGCATTGAGA CCGCAAGCTC TTTTTTTTAT GTCTAAAACG TCAAAATAAA AAGTAAACAC 60
AAAGAAAATG GTTGGCCnAG TGAAAACGTT TGAATCTGAC GAAACGAGAA AGAGC 115

(2) INFORMATION FOR SEQ ID NO: 4828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4828:

CCAAAATAGC CTTCATAATC CAAAACAGG CTCCTTTGAC TATAGATTTT CGTTTCTGGT 60
TCAGAAAGCT TTTGATTAAC TTTAAAGTAT nCCCAATTAT AAT 103

(2) INFORMATION FOR SEQ ID NO: 4829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GGACCGAACT GTCTCAGGAC GTTCTnAACC CATCTCGCGT ACCGCTTTAA TGGGCGAACA 60
GCCAACCCTT GGGACCGACT ACAGCCCCAT GATGCGATGA GCCGACATCG A 111

(2) INFORMATION FOR SEQ ID NO: 4830:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4830:

GTTGTTGGGG CCCCGCCGGC AAGGTTGACT AGAATTGAGA AAAGCTTGTT ACAACGCTAT 60
TTTCGTTTCAG TCAACnACTG CCAATATAAC TTTGTAGAGC ATTGA 105

(2) INFORMATION FOR SEQ ID NO: 4831:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4831:

ACATTGAGTC TTCGAGTCGT TGCATTTTCAC ACTGCCGnGA AAAGCCTCTA GATAGAAAAT 60
AGGTGCCCCGT ACCGCAAACC GACACAGGTA GTCAAGATGA GA 102

(2) INFORMATION FOR SEQ ID NO: 4832:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4832:

TnTAGAATG AACCGGCGAG TTACGATTTG ATGCAAGGTT AAGCAGTAAA TGTGGAGCCG 60
TAGCGATAAG GAGGTCTGAA TAGGGCGTTT AGTATTTGGT CGTAGCC 107

(2) INFORMATION FOR SEQ ID NO: 4833:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 144 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4833:

5 TGCAACTAAT GAAAAGTAGA GTTCCGGGGA GTTAAAACCA GTGACTGTTG ACCTTGTTGT 60
CTCCATTGGA ATGTACTACC TGATGCAAGA TAATTATCAT CACTTTGTTG ACGTGCTTnA 120
TTTTTCAGCAT CAATTTGATC AATC 144

(2) INFORMATION FOR SEQ ID NO: 4834:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4834:

20 GGCTCAGATG nACGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGCACCAGAA 60
GCTTGCTTCT CTGGATGTTA GCGCGGACG GGTGTAGTAA CACGTGGG 108

(2) INFORMATION FOR SEQ ID NO: 4835:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4835:

35 GACAATGGTA GGnGAGCGTT CTAAGGGCGT TGAAGCATGA TCGTAAGGAC ATGTGGAGCG 60
CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGCA GT 102

(2) INFORMATION FOR SEQ ID NO: 4836:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4836:

50 TTGCAGACTA CAATCCGGAA CTGGAGTAAC AACTTTATGG GATTTGnCTT GACCTCGCGG 60
TTTCGCTGGC CCTTTGGTAT TGTCCATTGT AGCACGTGTG TAGCCCCAAA 109

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4837:

CTCCACGTAA GCTAGCGCTC ACGTTTCAAA GGCTCCTACC TATCCTGGTA CAAGCTGTGC 60
CGGAATTTCA ATTTGCAnGC TACAGTAAAG CTCCACGGGG GTC 103

(2) INFORMATION FOR SEQ ID NO: 4838:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4838:

TCAAACACTC nCATACTGCT TTATTTTTCAT AAACAATATC ACTTTAACCA AAAAATATTT 60
GAATGTTAAA TAAACATTCA AAAGTGAATA CAATATGTCA CGTTATTCCA CATCTTCTGG 120
A 121

(2) INFORMATION FOR SEQ ID NO: 4839:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4839:

AAACCATGAA TTAAGAATCC AGAAACAGGA GATGTAGTTA GACCACCGGT CGATTAGCGT 60
ACCAAAATAT GGACCTGTAA AAGGAGACTC GATTGTAGAn AAAG 104

(2) INFORMATION FOR SEQ ID NO: 4840:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CCGTGGAGTT TATGTAGCCT GATATTGAAT TCGGCACAGT TGTACAGGTA GGTAGGAGCC 60
 TTGAAACGTG AGCGCTATTA GTGnAGGCGT GGTGGGTACT ACCCTAGCTG TGTGGCTTT 120
 CTAACCC 127

(2) INFORMATION FOR SEQ ID NO: 4841:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4841:

CATCCCAACC CGGCAAGGT TGACTAGAAT TGGAAAAAA CTTGGTTACA ACGTTATTTT 60
 CATTCACTCA ACTACTGCCA ATATAATATT GAAAACTATA GGACATTTAT TAGTGTTC 120
 GTTCT 125

(2) INFORMATION FOR SEQ ID NO: 4842:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4842:

TGGTACGGCA TCTCACCCGT CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAnGCGCTC 60
 CACATGATCC TTACGATCAT GACTTCAACG CCCTTAGAAC GCTCGTCC 108

(2) INFORMATION FOR SEQ ID NO: 4843:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4843:

TAATGAAGGT CTTCCGATCG TAAAACTCTG TTATTAAGnA GGAACATGTG TGTAAGTAGC 60
 TGTGCACATC TTGACGGTAC CTAATCAGAA AGCCACGGCT AACTACGT 108

(2) INFORMATION FOR SEQ ID NO: 4844:

(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4844:

10 CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGACCTGG GCAACGTTCT ACTCTAGCGG 60
AACCTAAGTT GGGCTACCAT CGACGnCTAA GAACCTTTCT TGA CT TGTGT ACAATCG 117

(2) INFORMATION FOR SEQ ID NO: 4845:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4845:

25 GACTGTTTAT CAAAAACACA GGTCTCTGCT AAACCGTAAG TGATGTATAG GGGGCTGACG 60
CCTGnCCGGG TTCTGGTAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAA 108

(2) INFORMATION FOR SEQ ID NO: 4846:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4846:

40 CAATATTTGA AGCGATTGGC TTGTCTCATG ATGTGATTGA TCGTTATTTT ACTGGGACAC 60
AGTCTAAGTT ATCTGGTATT TCGATTGATC AAATTnTGCC TGAAAAAGAC GCACAAGT 118

(2) INFORMATION FOR SEQ ID NO: 4847:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4847:

55 GATCCCCGGA CGGAGTGCTT AATGCGTTAC TGACAGCACT AAGGGGCGGA AACCCCTTAA 60

(2) INFORMATION FOR SEQ ID NO: 4848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4848:

CTGGCGATTA TGCTCTGTAA CGTGCTTTCC AATTTGGAAC GCACGTGnCC CTGCCCATAC 60
 CTACGGGACT TGACTTATAT TGTTTGGCTT TGTACGTCAT TTCAACAATA GACGCCCATG 120
 CCAGCAACGC GATTACC 137

(2) INFORMATION FOR SEQ ID NO: 4849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4849:

GTTTAGGCTC ATCTTAAGAT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTAATTACCG 60
 TTTTGGCAGA CGGCACTTGG TGGTACTTTA GAAGTCAAAG ACAAnGGGGGG GGGGGG 116

(2) INFORMATION FOR SEQ ID NO: 4850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4850:

TCCTTTTCGTG ACGGGCTCGG TAACTTACCC GACAAGGTAA TTTCGCTACC TTAGGnACCG 60
 TTATAGTTAC GGTCCGCCGT TTAAGTGGGC TTCGATTCGT ATCTTCGCAG CTATATCTCA 120
 CTCCT 125

(2) INFORMATION FOR SEQ ID NO: 4851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4851:

5 AAGTTGTATT TTAAAAATAG TTCTTTAAAT TATATACCCA CCACATTG TGGGAGAACC 60
TAAAAAAAAG CACTTTCCCC AAAAATGGGA AAGTGC 96

(2) INFORMATION FOR SEQ ID NO: 4852:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4852:

20 ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGnAT 60
GAACCGGCGA GTTCACGATT TAGATGCAAG GTTGAAGCAG 100

(2) INFORMATION FOR SEQ ID NO: 4853:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4853:

35 CCGACAGCGT AGnCGATGGA TAACAGGTTG ATATTCCTGG TACCACCTAT AATCGTTTTTA 60
ATCGATGGGG GACCCATAGG ATAGCGAACC TGCGATTGGA T 101

(2) INFORMATION FOR SEQ ID NO: 4854:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4854:

50 GGACATCTCC TAAGGCTAAA TACTCTCTAG TGACCGTAGT GAACCAGACC GTGAGGAAAAG 60
GTGAAAAnACC CCGGAGGGGA GTGAATAGAC CTGAAACCGT GT 102

(2) INFORMATION FOR SEQ ID NO: 4855:

55

(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4855:

10 ATAACCGCAA TTGGCGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA 60
CTTATCCCGT CCACACATAn CTACCCAGCT ATGCCGTTGG CACG 104

(2) INFORMATION FOR SEQ ID NO: 4856:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4856:

CTACTGTCTT CATTCTTTCA GTTCTTTTTT ACGGGTCTGT TTTCTAATTT GAGCACATCT 60
25 TCGATTCTTT ATCAAATGAC TACCAATTAA ATCTATTCCT CTnTGGTAAA TCGCTAACTC 120
CATCTCCTTA ACCCGGTA 138

(2) INFORMATION FOR SEQ ID NO: 4857:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4857:

40 TCAAACGnTT GTCATCTATT AAAGAAGTAG GTCTAGATAT ATCACGTACG TAATGTGTAA 60
TGGATGGCGC TATTGCTTTA GGTCATCCAT TAGGTGCTAC 100

(2) INFORMATION FOR SEQ ID NO: 4858:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4858:

55

CCTGTGTGTT TGATAAACAG TCGGTTGGGC CTATTCCTG CGGCTT

106

(2) INFORMATION FOR SEQ ID NO: 4859:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4859:

GTAAC TCGCC GGTTCATTCT AAAAAAGGGC ACGCCAATCA CCCATTAACG GGCTCCTGAA 60
CTACTTGTTA AGCAACACGG TTTCCAGGGT TCTATTTCCA CTTCCCCTTT CCGGGGTnGC 120
TTTTTCAACC TTTTCCCCC TCCACGGTTA CT 152

(2) INFORMATION FOR SEQ ID NO: 4860:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4860:

GCCCGTACCG CAAACCGACA CAGGTAGTCA AGATGAnGAA TTCTAAGGTG AGCGAGCGAA 60
CTCTCGTTAA GGAAC TCGGC AAAC TGA CCC CGTCACTTCG 100

(2) INFORMATION FOR SEQ ID NO: 4861:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4861:

CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTAA AAAGTAAGCG GATGAACTAA 60
AGGTAGCnGA GAAATTCCAA TCGAACCTGG AGATAGCTGG TTCT 104

(2) INFORMATION FOR SEQ ID NO: 4862:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4862:

TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60
 CCTCCTGCGT GCAAAGCAGG CGCTCTG 87

(2) INFORMATION FOR SEQ ID NO: 4863:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4863:

ACCGTTTGAT TTCTTATCTA ATTCAAGCTT ATTTAAACT CTTTATTCAC TCGGTTTTGG 60
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAnTTTTCA ATGTA 105

(2) INFORMATION FOR SEQ ID NO: 4864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4864:

AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60
 TGCCTTGCTG GATGATGCTA TGATATTGCA CATATCGAAT CAACAGTGGT GCATGAACCT 120
 GCAnTGGCT 129

(2) INFORMATION FOR SEQ ID NO: 4865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4865:

AAACCGCAAG GTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC 60
 TCGACTACnT GAAGCTGGAA ATCGCTATAA ATCGTAGATC 100

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4866:

GTGATAAGAT TAGCAGAAAA TGGATGGTGT TAAGAGAGTT AATTGGTTTG GnGGTATGCT 60
TATTTTAAAT GGCATTGTGT ACGAGAGCAT TAGAGTTTGT ACTTGTGAGG TTATT 115

(2) INFORMATION FOR SEQ ID NO: 4867:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 90 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4867:

ACACCACTCC TCATTAACT TCCAGCACCG CAGCAGGCGT CACCCCTATA CATCACCTTA 60
CGGTTTAGCA GAGACCTGTG TTTTGTATAA 90

(2) INFORMATION FOR SEQ ID NO: 4868:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4868:

CACGAACGAT TGTCTTGCGT GCGGGGATTA TCTGACACGG TACCGGTCAA ACAGTGAATC 60
GCTACTGCTC ATCAGGGATT ACAAACC 87

(2) INFORMATION FOR SEQ ID NO: 4869:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 165 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4869:

CGCTCACCTT AGAATCTATT TACTACTGGTG TTGGTAGGCA CTTTTTTCAA GCTTCCGATT 120
AACACATGAA AAGCTTCCAA AGTACTAGGA CGTTCAATAC ATGTA 165

5 (2) INFORMATION FOR SEQ ID NO: 4870:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4870:

AATATCATTT ATAACATTAA GTAATACTT TTTTATCTT GTCCATTTTA TTTTThAACC 60
AAAATTTGAT TAAAAAACTG CCTGGCAACG TTCTACTCTA GCGGAACTAA G 111

20 (2) INFORMATION FOR SEQ ID NO: 4871:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4871:

TAGCAGAGAC CTGTGTTTTT TGATAAACAG TCGCTTGGGC CTATTCCTG CGGCTCTTCT 60
GGGCGTTAAC CCTAAAGAGC ACCC 84

35 (2) INFORMATION FOR SEQ ID NO: 4872:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4872:

ACAGTAAAGC TCCACGGGTC TTTCCGTCCT GTCGCGGGTA ACTGCATCTT CACAGGTACT 60
ATGATTTCAC CGATCTCTCh ATGAACAGTG CCAAATCGTA C 101

50 (2) INFORMATION FOR SEQ ID NO: 4873:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4873:

5 GACAGGCGTA GGCGATGGAT AACAGGTTGT ATTCCTGTAC CACCTATGAT CGTTTTAATC 60
GATGGGGGGA AGCATAGGAT AGGCGAA 87

(2) INFORMATION FOR SEQ ID NO: 4874:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4874:

20 GGGAGAGCGC CTGCTTTGCA CGCAGGAGGT CAGCGGTTCTG ATCCCGCTAG TCTCCACCAT 60
TATTTGTACA TTGAAAATA G 81

(2) INFORMATION FOR SEQ ID NO: 4875:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4875:

35 TATGTTTCGA AATATCTTTA TCACTCTAAA ATGATATACA AGAAATCCAA GAAAAATAAG 60
CGAACTGAAT AAATAAGAT T 81

(2) INFORMATION FOR SEQ ID NO: 4876:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4876:

AACGCGTTAA ATCTTTTTAT AAAAGACGTA ACTTCATGTT AACGTTGCTT ATAAAAATGG 60
50 TGGAACATAG ATTAAGTTAT TAAGGGC 87

(2) INFORMATION FOR SEQ ID NO: 4877:

- (A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4877:

10 ACAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG TTCACATCGA 60
CGGGGAGGTT TgncCTCAAT GTGGCTCATC GGATCTTGGG G 101

(2) INFORMATION FOR SEQ ID NO: 4878:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4878:

25 ATTTATTAGG TGTACAAATG ACCACCGCAT CAACAAGTTT AAACAGCTCG CTAGGTGTCT 60
CAACTGCATG AGGTATATT 79

(2) INFORMATION FOR SEQ ID NO: 4879:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4879:

40 ACATCGTTTC AATGGGTCGC TAACGCTGCT AGGACATTAT AACAGACGTG TACAAAAAGA 60
AAATTGGTAT GGTAATTGTG GCA 83

(2) INFORMATION FOR SEQ ID NO: 4880:

45

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4880:

55 CTTTCATCCTG ATCCAGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA 60

(2) INFORMATION FOR SEQ ID NO: 4881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4881:

TTGTGCAGTT GCATCGCCAT TGATCAATAA CACGTTGAGC TGCAGTTATT TCAGTTTCTG 60
CTTCACGCTT CTTCGCATTA 80

(2) INFORMATION FOR SEQ ID NO: 4882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4882:

TCTGATGTGA AAGCCCACGG CTCAACCGTG GAGGGTCATT GGAAACTGGA AAAGTTGAGT 60
GCAGAAGAGG AAAGTGGGTT CCATGT 86

(2) INFORMATION FOR SEQ ID NO: 4883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4883:

TGATCGCATA TCTACGCAAC ATCGGCATAA GTnTGATGAC AAACAAGCTT CCATGACAAA 60
AGTAATGGAC GAATATCGCA TTTGGGGAAA GTCCTCTAAA AATGCCTTTT GAAGGAACGT 120
CGGTTAA 127

(2) INFORMATION FOR SEQ ID NO: 4884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4884:

AGTAGGAATC GAACCCACAC CAAAGTTTTG GAGACCTCTA TTCTACCTTG AACTATGCCC 60
CTATTAAAAA TAATAAAT 78

(2) INFORMATION FOR SEQ ID NO: 4885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4885:

CTCACTATTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60
GTGGATTGTC CTTTGGAAT GGGT 84

(2) INFORMATION FOR SEQ ID NO: 4886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4886:

GGTATCTGTT CACTCTCCG GTGGTGCACT TGCGACCAAC AATGGGTTGG AGATTGGATT 60
TCATCCTTCT CAATTAATCG TTGCCGTACT TTTCAANTGG TACCCCATCC AAAAGGG 117

(2) INFORMATION FOR SEQ ID NO: 4887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4887:

CGGATCTGGG AGGAAATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCACT 60
ACCGTGAGGA AAGGTGAAAA 80

(2) INFORMATION FOR SEQ ID NO: 4888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4888:

AATATGCAAG CACATGGTGA ATATGACGAG GTTGCAACTT CAACGGCGAA GATGATGGAA 60

10

GGCCTTACGT TTGCGTG 77

(2) INFORMATION FOR SEQ ID NO: 4889:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4889:

TCTTCTGGGC GTTAACCCTA AAGAGCACCC CTTCTCCCGA GTTACGGGGT CTTTGGCCGA 60

GTTCTTAAC GAGAGT 76

25

(2) INFORMATION FOR SEQ ID NO: 4890:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4890:

GTGGGGGCCC CAACATAGGA GCTGATTTTC TGTCAGCTTA CCATnATGTG GCAAGTTGGC 60

GGGGGCCCCC AAACCAAGGA GCTGGCTTTC TGTCACTTTA CCATTAATGT GGCAAGT 117

40

(2) INFORMATION FOR SEQ ID NO: 4891:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4891:

TTAATCCnCC TGCATATGAT GACTTTGTTG AACCGTCATT GCATACTTTC AACATGAATA 60

CGCTGAACAC CTTCACTTAC TGCATATCTT AGTTCCTCGG TCTGTCTTA 109

55

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4892:

CTCTTAACCT TGCAGCACCG GGCAGGCGTC AGCCCGTATA CATCACCTTA CGGTTTGCAG 60
AGACCGTGTG TTTTGTAGAA ACAGGTGC 88

(2) INFORMATION FOR SEQ ID NO: 4893:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4893:

TAGCGAATGA GATAAACGCG GCGGACTGTA AATCCGCTCC TTCGGGTTCG GCAGTTCGAA 60
TCTGCCCCCC TCCATTTATT ATTTTnAAAA AAAGCATAGT TC 102

(2) INFORMATION FOR SEQ ID NO: 4894:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4894:

CGAGCGATTC CGACTCAGAC AATGACTCGG AATTCAGATA ACGAATCTGA CTCAGACAGT 60
GACTCAGATT CCGACAGT 78

(2) INFORMATION FOR SEQ ID NO: 4895:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4895:

TTAGTATTCG CACTCACATG TCACATGCTT CACTCGACCT ATTACCTCAC ACTTGGGGAC 120
TTATACCGAG TnGGAATCTC A 141

(2) INFORMATION FOR SEQ ID NO: 4896:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4896:

GTTTCGGATTT AATTGATTTC ATTTGTTGCG TAATTTTCAGA AGCCATTTTA TGAAAAGAGT 60
GATTTAATTC ATAAATTTCT 80

(2) INFORMATION FOR SEQ ID NO: 4897:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4897:

GGTATGGCTG GCGCTTTACG TGCCACATTA GATTATGTCA CTGAGCGTAA GAAGTTCGGC 60
AAACCAATTA GTA 73

(2) INFORMATION FOR SEQ ID NO: 4898:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4898:

GTGCCGAGGA CCGGAATCGA ACCGGTACGG TGATCACTCA CCGCAGGATT TTAAGTCCTG 60
TGCGTCTGCC A 71

(2) INFORMATION FOR SEQ ID NO: 4899:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 116 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4899:

AGCCGCTGGA TTCCACGGTG TAAGCAGTAA GGCTGAGTAT TAGGCAAATC CGGTACTCGT 60
 TAAGGCTGGA GCTGTnGATG GGGAGAAGAC ATGTGTGCTT ACGTAGTGCG TGGTTT 116

(2) INFORMATION FOR SEQ ID NO: 4900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4900:

TTCCGGCCCC TGGCGGThTC CTAGGAGTTC CACGGAACCC CAGGATTTTG TAGGACCCCC 60
 CGGGCAGAGT CCCCTTCGAC TAAGAAAATC TCACATTCTT CAGGGACTTT TAC 113

(2) INFORMATION FOR SEQ ID NO: 4901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4901:

ACTTAATGGA TTGATTAAGT AGTGGGTTCT TAACATTAGG CCTCAGCTAA TGTGGTACTT 60
 AAAAAATAGGG AATACATG 78

(2) INFORMATION FOR SEQ ID NO: 4902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4902:

ATGGGACATG GTGTGCCTCC TTGCTATAGT CACCAGACAT ATGAATGTAA TTTATACATT 60
 CAAAACCTAGA TAGTAAGTAA AAGT 84

(2) INFORMATION FOR SEQ ID NO: 4903:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4903:

10 TTGTCGGGTA AGTTCCGACC CGCACGAAAG GCGTAACGAT TTTGGCACTG TCTCAACGAG 60
AGACTCGGTG 70

(2) INFORMATION FOR SEQ ID NO: 4904:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 151 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4904:

25 TAAGTTGGCT ACCATCGACG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60
TCCTCTTCTT GGCTCTGCTT CTATTTCCT CTAATGTGGC TTTTGTGTGT AATAAGTTAT 120
GCGCTTCGGT GTTATnGTGA AAAAGCGGTC A 151

30 (2) INFORMATION FOR SEQ ID NO: 4905:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4905:

40 TGACTTGTAG GCGCTGGTGG GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC 60
TTATCGTGGT GGGGA 75

45 (2) INFORMATION FOR SEQ ID NO: 4906:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4906:

55

ACTCAGACAG TGACTCAGAT CAGATAGTgn CTCGGATTCA GCGATTATTC AG

112

(2) INFORMATION FOR SEQ ID NO: 4907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4907:

GTAAAAACAC CCCAGCCAGG TCACTTTACG CCTACGCATC GCTTGTACAC GTGCTACTAA 60
AGGTTTACCA 70

(2) INFORMATION FOR SEQ ID NO: 4908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4908:

AGAAGATACA AATAAAGnTA AACCCAAATT ATTCAATTC GGTGGGACAC AATAGTGTG 60
ACTTTGAAGA AGATACACTT TCCCACCAAG TTAAGTGGGT CCATAATTGA AGGGTCCAAC 120
C 121

(2) INFORMATION FOR SEQ ID NO: 4909:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4909:

GGGAACAAAG TGGACAGGTG GTGCATGGTT GTCGTCAACT CGTGTCGTGA GATGTTGGGG 60
TTAAGTCCCCG 70

(2) INFORMATION FOR SEQ ID NO: 4910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4910:

5 GGACACCCGG AGAACTGAAA CATTAGTAC CCGGAGAAGA GAAGAAATTC GTTCCCTTAG 60
TAGCGGGACG AACGGGAGAG CCCAAACCAC AGCTTGTGnG 100

(2) INFORMATION FOR SEQ ID NO: 4911:

10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4911:

10 nTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGCTA TAGTCACCAG ACAAATAAC 60
20 TTACTTATTC ATGATACACG CTTAATTAAT AAGGTGCAAT AGTTAATTTT ACACTTTGAT 120
GTAAACTTTG GCACATCAGC TTTTAGTGTG TTTTCG 155

(2) INFORMATION FOR SEQ ID NO: 4912:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4912:

35 CCCGTCACAC CACGAGATTT GTAACACCCG AAAGCCGGTG GAGTGAACCT TTTAGGAGCT 60
AGCCGTCGA 69

(2) INFORMATION FOR SEQ ID NO: 4913:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4913:

50 TATGCTCTCC CAGCTGAGCT AATTCTCCGA TTAAAACTG CCTGGCAACG TTCTACTCTA 60
GCGGAACGT 69

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4914:

CAAATGCTTC TGTCAATTCG ATCAAATCAA TGTCTTCAAC AGATAGATTG CTGAGTGACA 60
ATACTTCAT 69

(2) INFORMATION FOR SEQ ID NO: 4915:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4915:

TATTTCCGGAG AGAACCAGCT ATTTCCAGGC TCGATTGGAA TTTCTCCGGT ACCCTCAGTT 60
CATCCGCTCA 70

(2) INFORMATION FOR SEQ ID NO: 4916:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4916:

TCACCCATTA ACGGGCTCTA ACTACTTGTA AGCACACGGT TTCAGGTTCT ATTTCACTCC 60
CCTTCCG 67

(2) INFORMATION FOR SEQ ID NO: 4917:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4917:

TCCACCGTTG ACTAAGGTTT CAGAGAGGCT CGTCCCTCTG GGTAGTCGGG CCTAAGCTGA 120
GGCGCACGTA GGCGATGATA CAGGTTATAT CCThACACCT A 161

(2) INFORMATION FOR SEQ ID NO: 4918:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4918:

GCACGTAGTT AGCCGTTGGC TTTCTGATTA GGTACCGGCA AGATGTGCAC AGTTACTTAC 60
ACATATGT 68

(2) INFORMATION FOR SEQ ID NO: 4919:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4919:

GAAAGCAAAT GTCTTCGTTG CAATTCGATC AAATCAATGT CTTCAACAGA TAGATTGCTG 60
AGTGACAATA CTTACAGG 78

(2) INFORMATION FOR SEQ ID NO: 4920:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4920:

AATTTGCTA CCTTAGGGAC CGTTATAGTT ACGGCCGACG TTTACTGGGG CTTCGATTG 60
TACTTCGC 68

(2) INFORMATION FOR SEQ ID NO: 4921:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4921:

AATCATAGTA CCTGTAAAGA TGCAGGTTAC CCGCAACAAG ACGGAAAGAC CCCGTGGAGC 60
TTTACTG 67

(2) INFORMATION FOR SEQ ID NO: 4922:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4922:

GGGAGCTGTA ATAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT 60
GTCATG 66

(2) INFORMATION FOR SEQ ID NO: 4923:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4923:

GTGGAGGCGC TGGTGGGATA CTACCCTAGC TGTGTTGGCT TTCTAACCCG CAACCACTTA 60
TCGTGGGTGG GAG 73

(2) INFORMATION FOR SEQ ID NO: 4924:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4924:

GAGGTCAGCG GTTCGATCCC GCTAGTCTCA CCATTTATTT TTTACACGAT GACATGAAAC 60
TGATGACATA TGCACCGTAA TTCCAAAAA 89

(2) INFORMATION FOR SEQ ID NO: 4925:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4925:

10 AATGGCATCG GAGTTGTCTG AATTCGGTAA CCCGAGAGGC CCCTCGTCCA AACAGGCTCT 60
ACCTCCAA 68

(2) INFORMATION FOR SEQ ID NO: 4926:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4926:

25 ACGAAAGGCG TAACGATTG GGCATGATC TCGACGAGAG ACTCGTGAAA ATCATAGATA 60
CCTGTGAAGA TGC 73

(2) INFORMATION FOR SEQ ID NO: 4927:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4927:

40 ATTTCTATTA ATTATTTGCA TAGAAATCAG CTTTTTTGAT ATGTATTTTA TAATGTACAG 60
CTCGTTGAG 69

(2) INFORMATION FOR SEQ ID NO: 4928:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4928:

55 AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACATCTC CTCTCAAATT TCCTACGCCC 60

(2) INFORMATION FOR SEQ ID NO: 4929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4929:

GGCGGGGCCC CAACACAGAG GCTGGCGGAA AGTGCAGCTT ACAATAGTGT GCAAGTTGGG 60
GTGGGTCCCC ACACAGAGAA ATT 83

(2) INFORMATION FOR SEQ ID NO: 4930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4930:

CTTGGTAGAG CACTTGTTTT GGGACCAAGG GGTCGCAGTT CGAATCCTGT CTTCCCGATT 60
ACTCTA 66

(2) INFORMATION FOR SEQ ID NO: 4931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4931:

AAGAAGCTTG TTATGCTGCA ACACCAGCAA TTCAAGTAGC TAAAGATTAT TTAGCAACTA 60
GACCG 65

(2) INFORMATION FOR SEQ ID NO: 4932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TGCAGAAGAG GAAAGTGGAA TTCCATGTGT AGGGTGAAAT GCGCATAGAT ATGGCAGGAA 60
CACCAGTGGG CGA 73

(2) INFORMATION FOR SEQ ID NO: 4933:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4933:

TCGCTATCCG AGTCTGGGTC GCTATCTGAG TCTGAGTCGC TATCTGAGTC TGAAATCGCT 60
GTCTG 65

(2) INFORMATION FOR SEQ ID NO: 4934:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4934:

GAGCATGTGG GTTTAATTCG AAGCAACGCA GAGAACCTTG ACCAAATCTT GGACATCCnT 60
TGACAACCTCT GAGAGATTAG AGCCTTGCCC CTTGCGGGGT AACAAATGTA CAGGTTGGTG 120

(2) INFORMATION FOR SEQ ID NO: 4935:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4935:

GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA GGCCGAGCAG GTACGGCGAT 60
GGATAACGGT TG 72

(2) INFORMATION FOR SEQ ID NO: 4936:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4936:

5 CACATCAGCG TCAGTTACAT ACCAGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT 60
CTGC 64

(2) INFORMATION FOR SEQ ID NO: 4937:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4937:

15 ATCACCTGGT GTAAACCAAT TAGTACGTGT ATATATCGTT CAAAACCGTA AAATTCATGT 60
20 TGGT 64

(2) INFORMATION FOR SEQ ID NO: 4938:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4938:

30 CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAACATC TAAGCATGAA GCCCCCTCAA 60
35 GAT 63

(2) INFORMATION FOR SEQ ID NO: 4939:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4939:

45 TAGAAATCAG CTTTTTTGCA TATGTATTTT ATAATGTACA GTCGTTGAG CTGCTATTTT 60
CCT 63

(2) INFORMATION FOR SEQ ID NO: 4940:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4940:

GGTAGTCGAA CTTACGTTCC GCTAGAGTAG AACTTGCCAG CAAATGACAA ATCGGAGAAT 60
TAGCTCAG 68

(2) INFORMATION FOR SEQ ID NO: 4941:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4941:

CTGAAACATC TTAGTACCCG GAGAAGAGAA AGAAAATTTCG ATTCCCTTAG TAGCGGCGAG 60
CG 62

(2) INFORMATION FOR SEQ ID NO: 4942:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4942:

TTACAACAAT GCAATTGGCG GGGCCCAACA TAGAACTGGC AATAGTTACT TTCAATAATG 60
TGCAAGTTGG GGTAGGGCCC AACACAGAA 89

(2) INFORMATION FOR SEQ ID NO: 4943:

45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4943:

AATGGACAAT ATGTCAACGT TAATTCCAAA AAACGGTAAC TATAATTTAC AACATTATT 60

55

(2) INFORMATION FOR SEQ ID NO: 4944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4944:

CCCGTGAAAG ATGATGAGGT TAATAGGTTT GAGGTGGAAG CATGGTGACA TGTGGAGCGT 60
GACGAATACG TAATTGA 77

(2) INFORMATION FOR SEQ ID NO: 4945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4945:

GAATAGGTCG ATGTATTTGG CGACCGAAAC CAGGAATCTA CCCTTGGTCA GGTGGAAGTT 60
CAGGTAACAC TGAAT 75

(2) INFORMATION FOR SEQ ID NO: 4946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4946:

ATCAGAAGGC ACACCCGAGA ATGAAACATC TAGTACCCGG AGAAGAGAAA GAAATTCGAT 60
TCCCTATAGC GGCGnCGAAA CGGAAGAGCC AACCACAGCT GCTTTGGTTT GACCCATCGG 120
TACAGCGCTG AACT 135

(2) INFORMATION FOR SEQ ID NO: 4947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4947:

GATTGGGCT CTTCCATTTC GCTCGCCGCT ACTAAGGGAA TCGAATTTC TTTCTCTTCC 60
T 61

(2) INFORMATION FOR SEQ ID NO: 4948:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4948:

GCTTTTGAGG AATTTAATAT CAATATATAT TCTGTGTATG AAAATATTTT TCATAAAAAT 60
TGTTTGAATC 70

(2) INFORMATION FOR SEQ ID NO: 4949:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4949:

CTTCGACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACCAAGT ACTAAACGCC 60
CTATTC 66

(2) INFORMATION FOR SEQ ID NO: 4950:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4950:

GGGTGTTACA AAATATCGTG GTGTGACGGG GCGGTGTGTA CAAGACCCCG GGTACGTTTT 60
TCACCGTAGG CATGCTGG 78

(2) INFORMATION FOR SEQ ID NO: 4951:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4951:

CCGCGATAAT AAAAAATAAT GGCGGAGGAA GAGGGATTCTG AACCCCGTG GCCCGTTAAG 60

10

G 61

(2) INFORMATION FOR SEQ ID NO: 4952:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4952:

ACTTATCTAG TTTTCAATGT ACAATGTCTT TTTAGTCAGC GCTCGCATAA GCAATATCAC 60

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TGTAACCA 68

(2) INFORMATION FOR SEQ ID NO: 4953:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4953:

ACTGACGCTG ATGTGCGAAA GCGTGGGGAT CAAACAGGAT TAGATACCCT GGTAGTCCA 59

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(2) INFORMATION FOR SEQ ID NO: 4954:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4954:

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CGTGAGCGCT AGCTGTACGT GGAGGCGCTG GTGGGATACT ACCCTAGCTG TGTGGGCTTT 60

(2) INFORMATION FOR SEQ ID NO: 4955:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 59 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4955:

AAGGCGTAAC GATTTGGGCA CTGTCTCAAC GAGAGACTCG GTGAAATCAT AGTACCTGT 59

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(2) INFORMATION FOR SEQ ID NO: 4956:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4956:

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AATAGGTGCC CGTACCGCAA ACCGACACAG GTAGTCAAGA TGAGAATTCT AAGGTGAGC 59

(2) INFORMATION FOR SEQ ID NO: 4957:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4957:

ACACGTTTAG TTCACGCGGG TTTTGCTTGG TAAAATCTAT ATTTTACTTA CTTATCTAGT 60

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TTTCAATGTA CAATTC 77

(2) INFORMATION FOR SEQ ID NO: 4958:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4958:

TGTCGTCAGC TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCTTAA 59

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(2) INFORMATION FOR SEQ ID NO: 4959:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4959:

5 GACTTGAACC CCCAACCTAC TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 59

(2) INFORMATION FOR SEQ ID NO: 4960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4960:

TATTAAGTGG TGACTTAGCG AGATGGACAA CGATGGCGAT ATATTTATTA TTGACCGCA 59

(2) INFORMATION FOR SEQ ID NO: 4961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4961:

30 ATGATTATCA TATTGCCTTA AATATCGCCA CAATTTTAGC GGGTGGTGAT TTACCAAGA 59

(2) INFORMATION FOR SEQ ID NO: 4962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4962:

CGCCGAAAAT TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACA 59

(2) INFORMATION FOR SEQ ID NO: 4963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TTAAGCTTAG TTGCCATCAT TAAGTTGGGC ACTCTAATGT TGA CTGCGG TGACAAACCG 60

(2) INFORMATION FOR SEQ ID NO: 4964:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4964:

TAGTTTTGGT ACGGTAACAA ATTTATTTGA AGAAACAATC TCAAATAAAG AATTGTTTG 59

(2) INFORMATION FOR SEQ ID NO: 4965:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4965:

AGTTCGGTCC CTATCCGTCG TGGGGCGTAG GAAATTTTAG AGGAGCTGTC CTTAGTACG 59

(2) INFORMATION FOR SEQ ID NO: 4966:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4966:

TACAAAGGGC AGCGAAACCG TGAGTCAAAG CAAATCCCAT AAAGTTGTTC TCAGTTCGG 59

(2) INFORMATION FOR SEQ ID NO: 4967:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4967:

CCATTGCAGC ACCGACAGCC ACACCATTTA TTTTTCGCT ATGTATATCG CATTAAACGT 60

(2) INFORMATION FOR SEQ ID NO: 4968:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4968:

GCCTCCGTTA CTTT TAGAGG CGACGCCAG TCAA ACTGCC CGCTGACACT GTCTCCCACC 60

(2) INFORMATION FOR SEQ ID NO: 4969:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4969:

CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC GCCGTTTACT GGGGCTTCG 59

(2) INFORMATION FOR SEQ ID NO: 4970:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4970:

CATCTGTCAC AGGTACTATG GATTTACCG GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60

TTACG 65

(2) INFORMATION FOR SEQ ID NO: 4971:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4971:

CTAGAGTTGG CATACCAGTC CGTCGCTAAG GAACCTTTCT TGACTTGATG ACAATCGACT 60

(2) INFORMATION FOR SEQ ID NO: 4972:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4972:

AGACCCCGTG GAGCTTTACT GTAGCCTGCA TATTCGAATT CGGCACAGCT TGTACAGGAT 60
AGGTAGG 67

(2) INFORMATION FOR SEQ ID NO: 4973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4973:

TGTGTACTTA AAAATATGAA TACATGAGTA AAACATCATGC ATAAGAAATA CTAATTTTC 58

(2) INFORMATION FOR SEQ ID NO: 4974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4974:

ACCTCCAATA ATCATCACTT GAGGCTAGCC CTAAAGCTAT TTCGGAGAGA ACCAGCTA 58

(2) INFORMATION FOR SEQ ID NO: 4975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4975:

GAGCCACAT CCTTTTCCAC TTGGCGTGTG TTTTGGGACC TTGGCTGGTG GTCTGGGCTG 60

(2) INFORMATION FOR SEQ ID NO: 4976:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4976:

TCACTAAGTC CGTCTTTTCGA CCCTGACTCG ACTTGTAGGT CTCGCAGTCA AGCTCCCTT 59

(2) INFORMATION FOR SEQ ID NO: 4977:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4977:

TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG TTTTAAAT 58

(2) INFORMATION FOR SEQ ID NO: 4978:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4978:

GTGAGGTACG TCCAGAATGG GGATTGGCTA AAAATGCATC ATTTATAATT GGACGACG 58

(2) INFORMATION FOR SEQ ID NO: 4979:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4979:

TCGCTATCTG AATCCGAGGT CGCTATCCGA ATCTGGAGTC GCTATCTGGA GTCTGGAATC 60

(2) INFORMATION FOR SEQ ID NO: 4980:

- (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4980:

10 AAGAAGGTAA TAATCCTGTA GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGAGTAC 58

(2) INFORMATION FOR SEQ ID NO: 4981:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4981:

GTGGTGTGTT AGGGCACTCT ATACGGGTTA CAAAGTACGA CATTAGACGG ATCATCTGGA 60

25 AAGATGAATC AAAGT 75

(2) INFORMATION FOR SEQ ID NO: 4982:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4982:

GTTCATTCATT TTCATTTATA TTTATATTAG TGTTAATCCA ATCATAGATT TATCTATA 58

(2) INFORMATION FOR SEQ ID NO: 4983:

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(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4983:

50 TGACAGCTAA CTATTGGCCA GCTTCTATGT TGGGGCCCCG CCAACTTGCA TTGTCTGTAG 60

A 61

(2) INFORMATION FOR SEQ ID NO: 4984:

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- (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4984:

10 GGTGTTTTTA AGTCTGATGT GAAAACCCAC GGCTCAACCG GTAGAGGTCA TTGGAAACTG 60
GAAA 64

(2) INFORMATION FOR SEQ ID NO: 4985:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4985:

25 CAGCATACAA TAATGTGCAA GTTGGTCGGG GCCCCAACAT AGAGAATTTC AAAAGAAAT 59

(2) INFORMATION FOR SEQ ID NO: 4986:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4986:

TGATGAAGGT CTTGGATCG TAAAACTCTG TTATTAGGGA AGAACATATG TGTAAGT 57

(2) INFORMATION FOR SEQ ID NO: 4987:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4987:

50 AAAGAATTTG CGCAAAACGC TATCGATACT GAAGGGCGTT CAATGATTAT CATGGGT 57

(2) INFORMATION FOR SEQ ID NO: 4988:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4988:

TTGTCACAAG TCAAGAAAGG TCTTTAGCGA CGATGGTAGC CAACTTACGT TCCGCTA

57

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(2) INFORMATION FOR SEQ ID NO: 4989:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4989:

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TAGGACCGTT ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAG

57

(2) INFORMATION FOR SEQ ID NO: 4990:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4990:

AAAGTCAACG TTAATTCCAA AAAACGTAAC TATAAGTTAC TAACATTATT TAGTATTTAT

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(2) INFORMATION FOR SEQ ID NO: 4991:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4991:

TCCACGGGGT CTTTCCATCC TGTCTCGGGT AACCTGCATC TTCACAGGTA CTATGATTTT

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(2) INFORMATION FOR SEQ ID NO: 4992:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs

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- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4992:

GTGCGGCTGG ATCACCTCCT TTCTAAGGAT ATATTCGGAA CATCTTCTTC AGAAGAT 57

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(2) INFORMATION FOR SEQ ID NO: 4993:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4993:

CCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACG 57

(2) INFORMATION FOR SEQ ID NO: 4994:

25

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4994:

CTGGTTTCGG GTCTACGACA AATACTAAAC GCCTATTCAG ACTCGCTTTC GCTACGG 57

35

(2) INFORMATION FOR SEQ ID NO: 4995:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4995:

CAAACCTCTCG TGGTGTGACG GCGGGTGTGG TACAAGCCCC GGGAACGTAT TCACCGTAGC 60

ATGCCGGTCT ACG 73

50

(2) INFORMATION FOR SEQ ID NO: 4996:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4996:

5 ACTAATTTCT ATAGGAAAAG TATTCTTTAT CGTCGTCCCA CCCCAACTCG CACATTATTG 60
TAAGC 65

(2) INFORMATION FOR SEQ ID NO: 4997:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4997:

20 ATTGGATTCC CAATTTCTAC AGACAATGCA GTTGGGGTGG GACGTCGAAA TAAATTTT 58

(2) INFORMATION FOR SEQ ID NO: 4998:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4998:

AACTTCAACA GGTTTTGCAG GTGGCGGTGC GACTGCAGGA AGACGTTAAA TTAATG 56

(2) INFORMATION FOR SEQ ID NO: 4999:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4999:

45 GGGCAGGCGT CAGCCCTATA CATCACCTTA CGGTTTAGCA GAGACCTGTG TTTTGT 56

(2) INFORMATION FOR SEQ ID NO: 5000:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5000:

TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG GAAACCTTAG TCAATC

56

(2) INFORMATION FOR SEQ ID NO: 5001:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5001:

GACGGGATTTC TCACCCGTCT TTCGCTACTC ACACCGGCAT TCTCACTTCT AAGCGC

56

(2) INFORMATION FOR SEQ ID NO: 5002:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5002:

CCTGTCGGCC TCAGCTTAGG ACCCGACTAA CCCAGAGCGG ACGAGCCTTC CTCTGG

56

(2) INFORMATION FOR SEQ ID NO: 5003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5003:

TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCA

56

(2) INFORMATION FOR SEQ ID NO: 5004:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5004:

(2) INFORMATION FOR SEQ ID NO: 5005:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5005:

GACATAGATT AAGTTATTAA GGGCGCACGG TGGATGCCTT GGCAC TAGAA GCCGATG 57

(2) INFORMATION FOR SEQ ID NO: 5006:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5006:

GGAACCACTA CATAATAAAT CATTAGTGGC TCTTTATCAT TCTGTCCCAC TCCCCTG 57

(2) INFORMATION FOR SEQ ID NO: 5007:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5007:

CGCTACGTTT TTCCTCAACA TTTAAGAAAA TAAAGAATGC TACAATTACG ATTGCAATCA 60
AACCAAAGA 69

(2) INFORMATION FOR SEQ ID NO: 5008:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5008:

AAAAGCTTGT TACAAGCGCT ATTTTCGTTT AGTCAACTAC TGCCAATATA ACTTCGT 57

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5009:

ACATCTTAGT ACCCGGAGAA GAGAAAGAAA ATTCGATTCC CTTAGTAGCG GCGAGC 56

(2) INFORMATION FOR SEQ ID NO: 5010:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5010:

GTTTGGACGA GGGGCCCTCT CGGGTTACGA TTCAGACAAA CTCCGATGCA ATTAATTTAC 60

TTGGG 65

(2) INFORMATION FOR SEQ ID NO: 5011:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5011:

TTTACTTGTA TTGGAATAAT TTCATCTTTG AACCGACCAT CACGTTGTGC GTCATA 56

(2) INFORMATION FOR SEQ ID NO: 5012:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5012:

CCTTATACAT CACCTTTACG GTTTTAGCAG AAACCTGTGT TTTTGTATAA ACAGTCGCTT 60

(2) INFORMATION FOR SEQ ID NO: 5013:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5013:

10 GGGCCCAACA CAGAAGCTGG CGAAAAGTCA GCATACAAAA TTGTGCAAGT TGGCGGGTCC 60
ACA 63

(2) INFORMATION FOR SEQ ID NO: 5014:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5014:

25 TAGGGTAGTA TCCCACCAAGT GGCCTCCACG TAAGCTAGCG CTTACGTTT CAAAGGCT 58

(2) INFORMATION FOR SEQ ID NO: 5015:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5015:

CAACTCCGAT GCAATTAATT TAACTTGGGA nCAGACATGG GTGATAAGGT CGTGTTTCGAA 60
40 GGGAACAGCC AGACACAGCT AAGTCCAGAT ATATGTAAGT GGAAA 105

(2) INFORMATION FOR SEQ ID NO: 5016:

45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5016:

CAAACGATTT ATTTATATGC TTATTTCTTT ATTTATTATT ATTACAATTA CATTTT 56

55

(2) INFORMATION FOR SEQ ID NO: 5017:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5017:

10 TCTGTAGAAA TTGGGGAATC CAATTTCTCT TGGTTTGGGT CCCATCCCCA ACTTGCACAT 60
TATTG 65

(2) INFORMATION FOR SEQ ID NO: 5018:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 56 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5018:

25 GGGGATGGGC CCCAACAAAG AGAAATTGGA TTCCCAATTT CTACAGACAA TGCAAC 56

(2) INFORMATION FOR SEQ ID NO: 5019:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5019:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTC 55

40 (2) INFORMATION FOR SEQ ID NO: 5020:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 58 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5020:

50 TACGGCGTTT AGTATTTGGT CGTAGCCGGA AACCAGGTGA TCTACCCTTG GTCAGGTT 58

(2) INFORMATION FOR SEQ ID NO: 5021:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5021:

TTGTGCGGGT CCCCCTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCCA 55

10

(2) INFORMATION FOR SEQ ID NO: 5022:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5022:

20

AGAGTTCACA TCGACGGGGA GGTTCGGCAC CTCGATGTCG GCTCATCGCA TCCTG 55

(2) INFORMATION FOR SEQ ID NO: 5023:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5023:

35

CCTTAGCTGG TGGTCTGGGC TGTTTCCCTT TCGAACACGG ACCTTATCAC CCATGGTC 58

(2) INFORMATION FOR SEQ ID NO: 5024:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5024:

45

TAAAGGCTAA ACTACCAATG TTTTCAATGG ATTTCCAAAA TGAATCATCT GGGAT 55

(2) INFORMATION FOR SEQ ID NO: 5025:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5025:

TCAAACCGGA GGGGTCATTG GAAACTGGAA AACTTGAGTG CAGAAGAGGA AAGTGAATT 60
5 CCA 63

(2) INFORMATION FOR SEQ ID NO: 5026:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5026:

GCTTGCGTAC CTAAAGAGCA CCCCTTCTCC GAATTACGGG GTCATTTTGC CGAGTTCCTT 60
20 AACG 64

(2) INFORMATION FOR SEQ ID NO: 5027:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5027:

AATACATAGC ATATCATAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGA 56

(2) INFORMATION FOR SEQ ID NO: 5028:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5028:

45 GGGCCCCTCT CGGGTTACCA ATTCAGACAA ACTCCGAATG CCAATTAATT TAACT 55

(2) INFORMATION FOR SEQ ID NO: 5029:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5029:

CGTAACTATA ACGGTCCTAA GGTAGCCGAA ATTCCTTGTC GGGTAAGTTC CGAC

54

(2) INFORMATION FOR SEQ ID NO: 5030:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5030:

ATCCCCGGGG CCCCAACACA GAGAATTTTCG AAAAGAAATT CTACAGGCAA TGCAAGT

57

(2) INFORMATION FOR SEQ ID NO: 5031:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5031:

TGCTTGGTAA AATCTATATT TTACTTACTT ATCTAGTTTT CAATGTACAA TTTC

54

(2) INFORMATION FOR SEQ ID NO: 5032:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5032:

TCCCTATCCG TCGTGGGCGT AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGA

54

(2) INFORMATION FOR SEQ ID NO: 5033:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5033:

(2) INFORMATION FOR SEQ ID NO: 5034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5034:

TATCTGAATC TGAGTCGCTG TCTGAATCTG AATCGCTATC CGAGTCTGAG TCGC

54

(2) INFORMATION FOR SEQ ID NO: 5035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5035:

CACCAGCAAT TCAATTAGCT AAAGATTATT TAGCAACTAG ACCGGAATGA AAAA

54

(2) INFORMATION FOR SEQ ID NO: 5036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5036:

CTACCATCGA CGCTAAGAGC TTAAGTTCTG TGTTCCGGCAT GGGAACAGGT GTGA

54

(2) INFORMATION FOR SEQ ID NO: 5037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5037:

CGGCGAGTTA CGATTTGATG CAAGGTAAAG CAGTAAATGT GGAGCCGTAG CGGAAG

56

(2) INFORMATION FOR SEQ ID NO: 5038:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5038:

10 GACCGGGATG GACATACCTC TGGTGTACCA GTTTGTCGTG CCAACGCATA AGCT 54

(2) INFORMATION FOR SEQ ID NO: 5039:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5039:

TTTCACCGAG TCTCTCGTTG AGCAGTGCCC AAATCGTTAC GCCTTTCGTG CGGG 54

25

(2) INFORMATION FOR SEQ ID NO: 5040:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5040:

35

TTATAACACG TATGCTTGGG GAGTGTAAATA AGCTTGATCA GAGATTCCnA TGGGAACCAG 60

CATGAGTTAT GTCATTTATC ATATGTGATC ATAGCATATC AAAGG 105

40

(2) INFORMATION FOR SEQ ID NO: 5041:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5041:

50

GGCACCTATT TTCTATCTAG AGGCTTTTCT CGGCAGTGTG GAAATCAACG ACTC 54

(2) INFORMATION FOR SEQ ID NO: 5042:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 54 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5042:

ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCG

54

10

(2) INFORMATION FOR SEQ ID NO: 5043:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5043:

20

CGTTCAGTCA ACTACTGCCA ATATAACATC GTAGAGCATA GAACATTGAT TTA

53

(2) INFORMATION FOR SEQ ID NO: 5044:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5044:

ACTAGAGAGT ATTTAGACTT AGGAGTGGTC CTCCCAGATT CCGACGGATT TCACGTGCT

59

35

(2) INFORMATION FOR SEQ ID NO: 5045:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5045:

TTTCGTCGTC CCACCCCAAC TTGCACGCTA TTGTGAGCTG ACTTTTCGCC AGCTTCTGTG

60

TT

62

50

(2) INFORMATION FOR SEQ ID NO: 5046:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5046:

CGTCATCCCC ACCTTCCTCC GGTTTGTAC CGGCAGTCAA CTTAGAGTGC CCA

53

(2) INFORMATION FOR SEQ ID NO: 5047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5047:

TATTTATTAA ACCTAATAAA GATGAATTAG AAGTGATGTT TAATACAACA GTG

53

(2) INFORMATION FOR SEQ ID NO: 5048:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5048:

CCTCGGCACC ATTTTCAATA AAAACATATG CGCCCGTAGC TCAATTGGAT AGA

53

(2) INFORMATION FOR SEQ ID NO: 5049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5049:

AAATGGCCAA CTTAAGCCAG GATACAATTT ACAAATAGCG ACAAATTCTC AATGTGTTT

59

(2) INFORMATION FOR SEQ ID NO: 5050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CGAAAGACAC nCACAAGATT AATAACGCGT TTGAGTCTTT TTATAAGAC GTACTTCATG 60
TTACGTTGAC TTAAAGATGG TGGAACATAG TTAGTTTTAG GGCCACGGGG G 111

(2) INFORMATION FOR SEQ ID NO: 5051:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5051:

ACGTTGACAT ATTGTCATTC AGTTTTCAAT GTTCATTAAT GTTCAATCTC TTT 53

(2) INFORMATION FOR SEQ ID NO: 5052:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5052:

CTGAATTCGG TAACCCGAGA GGGCCCCTCG TCCAAACAGT GCTCTACCTC CAA 53

(2) INFORMATION FOR SEQ ID NO: 5053:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5053:

TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC CGG 53

(2) INFORMATION FOR SEQ ID NO: 5054:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5054:

(2) INFORMATION FOR SEQ ID NO: 5055:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5055:

TAGGGCTAGC CTCAAGTGAT GATTATTGGA GGTAGAGCAC TGTTTGGACG AGG 53

(2) INFORMATION FOR SEQ ID NO: 5056:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5056:

ACTGCTTTGA AATGTTGTTG TCTCAGTTAA TATTCAATTG CTTTTCTTTT GCATAATTGA 60
CAA 63

(2) INFORMATION FOR SEQ ID NO: 5057:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5057:

CTATGTTGGG GCCCCGCCAA CTTGCATTGT CTGTAGAATT CCTTTTCGAA ATTC 54

(2) INFORMATION FOR SEQ ID NO: 5058:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5058:

CTGAATCCGA GTCGCTATCC GAGTCTGAGT CGCTATCTGA GTCTGAATCG CTG 53

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5059:

TTTGGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG TGATGTCAA

59

(2) INFORMATION FOR SEQ ID NO: 5060:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5060:

AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT AAAAAACAGC AGT

53

(2) INFORMATION FOR SEQ ID NO: 5061:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5061:

TTAAAGAGTG CGTAATAGCT CACTAATCGA GTGACAATGG CGCCGAAAAT GTACC

55

(2) INFORMATION FOR SEQ ID NO: 5062:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5062:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTCGC ACATCAGCGT CA

52

(2) INFORMATION FOR SEQ ID NO: 5063:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5063:

TCGCCAAGCC ATTTTCTTT GTGTTCTTT TTATTTTGAC GTTTTAGACA TA 52

10 (2) INFORMATION FOR SEQ ID NO: 5064:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5064:

CTCAAGCTCC CTTGTGCCTT TACACTCTAT GTGTGCTTC CGACCGTTCT GGGGGGAACT 60

TTGGAGCGCC TCCGTT 76

25 (2) INFORMATION FOR SEQ ID NO: 5065:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5065:

CCACCGCTTG TGCGGGTCCC CGTCAATTCC TTTGAGTCGC AACCTTGCGG TCGT 54

(2) INFORMATION FOR SEQ ID NO: 5066:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5066:

TCCCCGGGCT AAACATATTA CCGAAGCTGT GGATTGTCCT TTGGACAATG GTAGG 55

50 (2) INFORMATION FOR SEQ ID NO: 5067:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5067:

GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AA

52

(2) INFORMATION FOR SEQ ID NO: 5068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5068:

CGGACACCAG AAGTACCAAG CGAGCCGGAA ACACCAACAC CACCGACACC AGACGTACAA

60

GCGAGCGGAA ACAACAACAA CG

82

(2) INFORMATION FOR SEQ ID NO: 5069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5069:

TCCATAACGT GCTGTATCTG TAGCAATAAC TAATACTTTT TCATTTCGGTC TA

52

(2) INFORMATION FOR SEQ ID NO: 5070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5070:

CGACTCGAAG ACTCAATGTC TTCTCCCAT CACAGCTCAG CCTTAACGAG TA

52

(2) INFORMATION FOR SEQ ID NO: 5071:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5071:

GCGATGGATA ACAGGTTGAT ATTCTGTAC CACCTATAAT CGTTTTAATC GA

52

(2) INFORMATION FOR SEQ ID NO: 5072:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5072:

CACTTCACCA CAGCCGCCAT GGCATGGGCA GTAGGAATCG AACCCACACC AAA

53

(2) INFORMATION FOR SEQ ID NO: 5073:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5073:

GTCCAGACTC CTACGGGAGG CAGCAGTAGG GAATCTTCCG CAATGGGCGA AA

52

(2) INFORMATION FOR SEQ ID NO: 5074:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5074:

TGTTGGCTTA GAATCAGCCA TCATTAAAG AGTGCCTAAT AGCTCACTAG TCGC

54

(2) INFORMATION FOR SEQ ID NO: 5075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5075:

AAACTTCCCT TTGG

74

(2) INFORMATION FOR SEQ ID NO: 5076:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5076:

TGAGCTAATC AGACATCATA ATTTTATGG AGAGTTTGAT CCTGGCTCAA GAT

53

(2) INFORMATION FOR SEQ ID NO: 5077:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5077:

GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTC CGCTAGAGTA GA

52

(2) INFORMATION FOR SEQ ID NO: 5078:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5078:

GGGTAAGTTC CGACCCGCAC GAAAGGCGTA ACGATTTGGG CACTGTCTCA AC

52

(2) INFORMATION FOR SEQ ID NO: 5079:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5079:

ATTAATCCAT TGTGCCACAA GTGCCGGACC AGAAATGATG GTATTTAATA AT

52

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5080:

AATAGCGACG AATCACACCT TCTGCGGCAC CACGGAATAA TACACCATGT GG

52

(2) INFORMATION FOR SEQ ID NO: 5081:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5081:

CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAAGCGCTC CACATGTCCT TA

52

(2) INFORMATION FOR SEQ ID NO: 5082:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5082:

CAGACAGCGA CTCAGATCAG ATAGCGATCG GACTCAGACA ACGACTCAGA TTCAGA

56

(2) INFORMATION FOR SEQ ID NO: 5083:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5083:

AGGGTATGAT CCATCCCGGG TCCTCTCGGT ACTAAGGGAC AGCTCCTCTC AAATTTCTTA

60

CG

62

(2) INFORMATION FOR SEQ ID NO: 5084:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5084:

10 GTGTACCAGT TGTCGTGCCA ACGGCATAGC TGGGTAGCTA TGTGTGGACG AG 52

(2) INFORMATION FOR SEQ ID NO: 5085:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5085:

TTGCTTACGC TTGCTATAGC CAATATATAG ATGTTGGAGG GGCAGATTC GAATGCGAAC 60

CCGAGGAGCG GATTAACA 78

25

(2) INFORMATION FOR SEQ ID NO: 5086:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5086:

ACTGACGCTG ATGTGCGAAG CGTGGGGATC ACACAGGATT AGATACCCTG GT 52

(2) INFORMATION FOR SEQ ID NO: 5087:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5087:

50 AAGTTGTTCT CAGTTCGGAT TGTAAGTCTGC AACTCGACTA CATGAAGCTG G 51

(2) INFORMATION FOR SEQ ID NO: 5088:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 51 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5088:

AATAC TT TAA AAAAATAAGA CACTTTGGCC AACTTAAGCC AGGATACAAT T 51

10 (2) INFORMATION FOR SEQ ID NO: 5089:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5089:

20 AGAACGTAAA TTAAATCCTG ATTTAGCACC AGGGACAGAA AAAGTAACAA G 51

(2) INFORMATION FOR SEQ ID NO: 5090:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5090:

CCGCTACCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTTCGGTC C 51

35 (2) INFORMATION FOR SEQ ID NO: 5091:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5091:

CATGGGTGAT AAGGTCCGTG TTCGAAAGGG AAACAGCCCA GACCACCAGC T 51

(2) INFORMATION FOR SEQ ID NO: 5092:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5092:

TTGTGCGGAT CCCCCTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCC

55

(2) INFORMATION FOR SEQ ID NO: 5093:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5093:

CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG A

51

(2) INFORMATION FOR SEQ ID NO: 5094:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5094:

ACGAATACTA ATCGATCGAA GACTTAATCA AAATAAATGT TTTGCGACAA A

51

(2) INFORMATION FOR SEQ ID NO: 5095:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5095:

AATCGTTGTT ACCTTCATTA TACCACTTAC TTGTGGAGTG ATCTTCTTCA AAGTAACACT

60

ATTGTGCCAC CGATTGA

77

(2) INFORMATION FOR SEQ ID NO: 5096:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

TTCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CG

52

(2) INFORMATION FOR SEQ ID NO: 5097:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5097:

GGGTCTGTTT TCTAATTGA GCACAATCTT CGTTCTCAAT AGAATGATTT A

51

(2) INFORMATION FOR SEQ ID NO: 5098:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5098:

CTGTAGAAAT TGGGAATCCA ATTTCTCTAT GTTGGGGCCC ACACCCCAAC T

51

(2) INFORMATION FOR SEQ ID NO: 5099:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5099:

CTGTGGATTG TCCTTTGGCA TGAGATAGGA GAGCGTTCTA AGGGCGTTGA A

51

(2) INFORMATION FOR SEQ ID NO: 5100:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5100:

GGTTCAGAAC GTCGTGAGAC AGTTCGGTCC CTATCCGTCG TGGGCGTAGG A

51

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5101:

TGACTGATAC GATCAATGCG CTTGTAACAA GCTTTTTTCA ATTCTAGTCA GGGGCCCCAA 60
CACA 64

(2) INFORMATION FOR SEQ ID NO: 5102:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5102:

TATTTGCATT TATATTGACG TTTTAAACAT AAAAAAAGAA ACCTTGCGGT CTCAATGG 58

(2) INFORMATION FOR SEQ ID NO: 5103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5103:

ATTACCATTT TGGTATACCA CATCGTTATT CAACACATTA TCTTTTACTT 50

(2) INFORMATION FOR SEQ ID NO: 5104:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5104:

GGACACTGCT CCCTCAGGAG TCTCGCCATT AATACTACGT ATTAACATGT AAT 53

(2) INFORMATION FOR SEQ ID NO: 5105:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5105:

ATTCTCTCTT TTTCTACAAT CGAGTCTCCT TTTACAGGTC CATATTTTGT

(2) INFORMATION FOR SEQ ID NO: 5106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5106:

TGGTCAAGCG GTTAAGACAC CGCCCTTTCA CGGCGGTAAAC ACGGGTTCGA

(2) INFORMATION FOR SEQ ID NO: 5107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5107:

TTTTTAGCAG TAATTGCCAC ATCTGTGTGA CGATAATGAT ATGCGACAGT

(2) INFORMATION FOR SEQ ID NO: 5108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5108:

CAAGCCATTT TTCTTTGTGT TTACTTTTTA TTTTGACGTT TTAGACATAA

(2) INFORMATION FOR SEQ ID NO: 5109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5109:

AGCCGATGAA GGACGTTACT AACGACGATA TGCTTTGGGG AGCTGTAAGT

50

(2) INFORMATION FOR SEQ ID NO: 5110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5110:

ATCCATAACG TTTGGTATCT GTAGCAATAA CTAATACTTT TTCATTTCGGT CTA

53

(2) INFORMATION FOR SEQ ID NO: 5111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5111:

CCCTTAGTAC TGCAGCTAAC GCATTAAGCA CTCCGCCTGA GGAGTACGAC CTC

53

(2) INFORMATION FOR SEQ ID NO: 5112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5112:

GGAGTCAAAG TCCGTTGCCT TACCGCTTGG CTATAGCCCA ATATATAGAT

50

(2) INFORMATION FOR SEQ ID NO: 5113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AGAnTTTCTT TTCGAAATTC TTTATGTTGG GGCCCCGCCA ACTTGCATTG

50

(2) INFORMATION FOR SEQ ID NO: 5114:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5114:

GCTGTGATGG GGAGAAGACA TTGTGTCTTC GAGTCGTTGA TTTCACACTG

50

(2) INFORMATION FOR SEQ ID NO: 5115:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5115:

CTTGATTAAC TCATTATCAA GTTATGCACG TGTAATGAA TTCGGCTTTA TCGAA

55

(2) INFORMATION FOR SEQ ID NO: 5116:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5116:

GTACTTAAAA AATGAATACA TGAGTAAAGC TCATGGCATA AGAAATACTA

50

(2) INFORMATION FOR SEQ ID NO: 5117:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5117:

CAGAATCAGA TAGCGACTCA GAATCAGATA GTGAGTCAGA TTCAGCAGTh

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5118:

CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACnAA

(2) INFORMATION FOR SEQ ID NO: 5119:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5119:

AATCGTCGAA ACTTAATCAA AATAAATGTT TTGCGACAAA TCACTTTTAC TTACTATCTA

(2) INFORMATION FOR SEQ ID NO: 5120:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5120:

CCGAAGTTTA CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG

(2) INFORMATION FOR SEQ ID NO: 5121:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5121:

ATAATCCTGT AGTCGAAAAT GTTGTCTCTC TTGAGTGGAT CCTTAGTACG CCGGGGCACG

T

(2) INFORMATION FOR SEQ ID NO: 5122:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5122:

10 TAGCGACTCA GATTGAGACA GCGATTGAGA CAGCGACTCA GACTCAGATA 50

(2) INFORMATION FOR SEQ ID NO: 5123:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5123:

TATTTGTAAA TTGTATCCTG GCTTAAGTTG GCCATTTTTC ATATGGTCTT 50

(2) INFORMATION FOR SEQ ID NO: 5124:

25

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5124:

35 CACGAGCTGA CGACAACCAT GCACCACCTG TCACTTTGTC CCCCAGAGAAG GTCTCTATCT 60

(2) INFORMATION FOR SEQ ID NO: 5125:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5125:

AGAACACATT GCAGTCTTCG AGTCGTTGAT TTCACACTGC CGTAGTAAAA GCCTCTAGAT 60

50 AGAA 64

(2) INFORMATION FOR SEQ ID NO: 5126:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5126:

GGACGACATT AGACGAATCA TCTGGAAAAG ATGAGTCAAA GAAGGTAATA GTCCTGT

57

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(2) INFORMATION FOR SEQ ID NO: 5127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5127:

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GTCCTTAGTA CGAGATGACC GGGATGGACA TACCTCTGGT GTACCAGTTG

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(2) INFORMATION FOR SEQ ID NO: 5128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5128:

GCCGATTTTA GCAGTTGTTG CTTCGTTCAA TTTTATGGGG CCATTTATGG

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(2) INFORMATION FOR SEQ ID NO: 5129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5129:

45

TCCACACATA GCTACCCAGT CTATGCCGTT TGCCTACAA CTGGTACACC A

51

(2) INFORMATION FOR SEQ ID NO: 5130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5130:

CTCAGTTGGT TGAGCATCTG ACTTTTAATC AAAGGGTCAA GGGTCGAATC CTCTTTT

57

(2) INFORMATION FOR SEQ ID NO: 5131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5131:

TGATATTCAC TTCAATGTGA TCAATATTAG TGCCATCTAT GACATCTGCC A

51

(2) INFORMATION FOR SEQ ID NO: 5132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5132:

TCCTGTAGTC GAACGTGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG A

51

(2) INFORMATION FOR SEQ ID NO: 5133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5133:

ACTCAGACAT TGGATTCAGA TTCAGACAGC GACTCAGATT CAGATAGCGA CTCAGATTC

59

(2) INFORMATION FOR SEQ ID NO: 5134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5134:

(2) INFORMATION FOR SEQ ID NO: 5135:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5135:

CAATACnAAG GGCAGCGAAA CCGTGATTCA AGCAAATCCC ATAAAGTTGG 50

(2) INFORMATION FOR SEQ ID NO: 5136:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5136:

GAAGCTGGCG AAAAGTCAGC TTACAAAATG TGCCAGTTGG CGGGGGCCCA AC 52

(2) INFORMATION FOR SEQ ID NO: 5137:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5137:

TTGTAAGGAA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGAnT 50

(2) INFORMATION FOR SEQ ID NO: 5138:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5138:

CTGTACAAGC TGTGCCGATA TTTCAATATC AnGnTACAGT AnAGCTCCAC 50

(2) INFORMATION FOR SEQ ID NO: 5139:

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5139:

10 GGTTCGAATC CTGTCTTCCC GATATACTGT AATTATTATG GGGGCTTTGC TC

52

(2) INFORMATION FOR SEQ ID NO: 5140:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5140:

GCTACTGAAC CTATAAAATG TATGATGGCG GTCTCGAGGG AATCGAACCC AGATCT

56

25 (2) INFORMATION FOR SEQ ID NO: 5141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5141:

35 AGGAGGCTCG TCCGCTCTAG GTTAGTCGGG TCCTAAGCTG AGGCCGACAG TA

52

(2) INFORMATION FOR SEQ ID NO: 5142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5142:

CACGCTTTTCG ACATCAGCGT CAGTTACAGA CCAGAAAGTC GCCTTCGCAC TGGTGT

56

50 (2) INFORMATION FOR SEQ ID NO: 5143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5143:

CTCCTAAAC AATTACATC CAAACCTTCA TCACTCACGC GCGTTGCTC CGTCAGCTTT 60
CGCCATTGCG AAGAT 75

(2) INFORMATION FOR SEQ ID NO: 5144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5144:

GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT 55

(2) INFORMATION FOR SEQ ID NO: 5145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:

GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG 53

(2) INFORMATION FOR SEQ ID NO: 5146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:

AGCTGTGGAT TGTCCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T 51

(2) INFORMATION FOR SEQ ID NO: 5147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5147:

CTCTTTGATC CGTAGTCAAA CGCTCTATCC AATTGAGCTA CGGGCGCATA

50

(2) INFORMATION FOR SEQ ID NO: 5148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5148:

GAACTAATTC TCCAAAATAA TGACTCCTAC AGGAACTCGA ACCCGTATAA CCGCCGTAAA

60

(2) INFORMATION FOR SEQ ID NO: 5149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5149:

AAAGCACACC CGGAAAAC TG AACATCTTA AGTACCCGGA GnaAGAGAAA

50

(2) INFORMATION FOR SEQ ID NO: 5150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5150:

GTAAGTTCGC ACTACCATCG ACGCTAAGGG AGCTTAACTT CTGTGGTTTCG GCATGG

56

(2) INFORMATION FOR SEQ ID NO: 5151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5151:

(2) INFORMATION FOR SEQ ID NO: 5152:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5152:

CTATTCTCTG TGTCGGGCTC ACCCCAAC TT GCACACTATT GTAAGCTGAC TTTCTCTCCA 59

(2) INFORMATION FOR SEQ ID NO: 5153:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5153:

TAACCACATC ATTCGGATAC TGTTTCATGGA AGTAATTTCT CTATTCTTCG GACCAGGAAA 60
ATACA 65

(2) INFORMATION FOR SEQ ID NO: 5154:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5154:

CCATATGTGT CAGTCACTGT GCACATCTTG ACGGTACCTA ATCAGACAGC CACGGCTAAC 60
TCCGTGCCAG CCGCCGCGGT ACTACGTGGT G 91

(2) INFORMATION FOR SEQ ID NO: 5155:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5155:

(2) INFORMATION FOR SEQ ID NO: 5156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5156:

GACTCTGGGA GGACCATCTC CTAAGGCTAA ACTACTCTCT CGTGACCGAT AGTGAACC

58

(2) INFORMATION FOR SEQ ID NO: 5157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5157:

TTGTAAGTCC GGTATAGGAG TGTCTACAA CCCCACCAAG CAAGCTTGT G

51

(2) INFORMATION FOR SEQ ID NO: 5158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5158:

TAGTnACCGn TAGTGAACCA TTACCGTGAG GGAAAGGTGA AAAGCACCCC

50

(2) INFORMATION FOR SEQ ID NO: 5159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5159:

TTCGCTCGCC GCTACTCAAG GGAATCGCAT TTCCTTTCTC TTCCTCCGGG T

51

(2) INFORMATION FOR SEQ ID NO: 5160:

- (A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5160:

10 AACTGGAGAA ACAACTTTAT GGGGTTTGCT TGAACCTCGC GGTTTCGCTG CCCTTTGTAT 60
T 61

(2) INFORMATION FOR SEQ ID NO: 5161:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5161:

25 AGACCTCTGC CTTACCACTT GGCTATGCGC CAATAACTGG GCTACCTGGA T 51

(2) INFORMATION FOR SEQ ID NO: 5162:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5162:

CCGCTCACTT TTCAACGTAA GTCGGATCGG TCCTCCATTC AGTGTCACCT GAACT 55

(2) INFORMATION FOR SEQ ID NO: 5163:

40

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5163:

50 CTTGATCTGT ATTTAAAATG ATATTTTCTA TCTTTTCTTT ATTATTAACG TCTATGACGT 60
CGTAGTATAA GATTCCGTGT A 81

(2) INFORMATION FOR SEQ ID NO: 5164:

55

- (A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5164:

10 GTTCGAATCC CGTCTTCTGC TCCATTATTT TGCCGGGGTG GCGGCAACTC TCACACGCAC 60
AG 62

(2) INFORMATION FOR SEQ ID NO: 5165:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5165:

25 CAGGGGTCTT TCGTCCTGTG TGGGTAAGT CATCTTCACA GGTACTATGA TTTCA 55

(2) INFORMATION FOR SEQ ID NO: 5166:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5166:

35 AAGCTGAGGC CGACAGCGTA GGCGATGGAT GACAGGTTGA TATTGCCGGT ACCACCCGAT 60
40 AA 62

(2) INFORMATION FOR SEQ ID NO: 5167:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5167:

50 CTTGCGTCTC CAGTTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA CG 52

(2) INFORMATION FOR SEQ ID NO: 5168:

55

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5168:

10 TCGTCCGCTA TCTCCACCAT TATTTGTACA TTGAACTAG ATAAGTAGTA AATATA 56

(2) INFORMATION FOR SEQ ID NO: 5169:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5169:

CTTGGACGTC GGTGGGTAGT CGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCA 55

(2) INFORMATION FOR SEQ ID NO: 5170:

25

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5170:

35 CTACTGCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCA TA 52

(2) INFORMATION FOR SEQ ID NO: 5171:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5171:

GGGCTTnGGA CATTAGTTC TnAGGCAATG TAAAAAAGCT GATTCTATT 50

(2) INFORMATION FOR SEQ ID NO: 5172:

50

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5172:

AAATTACATG TTAATACGTA ATTAATGGCG AGACTCCTGA GGAACCATTG CCATTCGAAG

60

(2) INFORMATION FOR SEQ ID NO: 5173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5173:

GTTTTATTTT TTAAAGTAT GTAAAAGTAA AATTACATGn TAATACGTAn

50

(2) INFORMATION FOR SEQ ID NO: 5174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5174:

CAACTCTCGT TAAGGAACTC GGCAAAATAC CCCGTAAGTT CGGAGTAGGT CTCTTTA

57

(2) INFORMATION FOR SEQ ID NO: 5175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5175:

GGAAACTGGA ATAAATAAAC ATTCAATTGA GCGCATCAGT ATTAGGATTC ACTCTAAAAA

60

(2) INFORMATION FOR SEQ ID NO: 5176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GTAACGGACG CGCTCAAAGG TTCCCTCACA ATGGTTGGAA ATCATTGATA

50

(2) INFORMATION FOR SEQ ID NO: 5177:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5177:

AGTTACGTTT TTTTATAAAG AGGTTTGAGA CGCGTTATTA ATCTTGTGAG

50

(2) INFORMATION FOR SEQ ID NO: 5178:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5178:

GTGTGGATCC TGAGTACGAC GGAGCACGTG ACAATTCCGT CGGCAATCTG GGG

53

(2) INFORMATION FOR SEQ ID NO: 5179:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5179:

CGGTAAGTTC ATACCTTTTA ACATATTTTG CATTGATTG CGTTTACCTT TTTTACCTTT

60

ACCGCCACCA GTGAACTGTT TCA

83

(2) INFORMATION FOR SEQ ID NO: 5180:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5180:

TTTAAA

66

(2) INFORMATION FOR SEQ ID NO: 5181:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5181:

GTTCGGTAAC TCGAGCGGGT CTCATAACCC GTAGGTCGGG TGGTTCAAAT CCGTCCTCCC
GCAATAT

(2) INFORMATION FOR SEQ ID NO: 5182:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5182:

TAGCGGTGAA ATGCGCAGAG ATATGGAGGA ACACCAAGTAG CGAAGGCAAC TTTCT

(2) INFORMATION FOR SEQ ID NO: 5183:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5183:

GAATTCCATG TGTAGCGGTG AAATGCGCAG AGATATGnAC GAACACCAAT

(2) INFORMATION FOR SEQ ID NO: 5184:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5184:

CC

62

(2) INFORMATION FOR SEQ ID NO: 5185:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5185:

GAGACCTTGT CGGTCCATAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGT

(2) INFORMATION FOR SEQ ID NO: 5186:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5186:

CCATCATTAAGTTGGGCACT CTAAGTTGAC TGCCGnGnC ACCnAAGAAG

(2) INFORMATION FOR SEQ ID NO: 5187:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5187:

TTAATACGTT GCAATCCAAT CGCAGCTTC GCCTATCCTA CTGCCnTCCC

(2) INFORMATION FOR SEQ ID NO: 5188:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5188:

AGTCGCTATC CGAATCTGAG TCGCTATCTG AGTCTnAGTC GCTAnnCCAG

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5189:

ATAGATGCCC TTACCGCAAA CCGACACATG TAGTCAATAT GATAATTCTA AGGT

54

(2) INFORMATION FOR SEQ ID NO: 5190:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5190:

CTTTAATGGG CGAACAGnAC CCTTGGACCG ACTACAGCCC AGATCGATGA

50

(2) INFORMATION FOR SEQ ID NO: 5191:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5191:

ACATAGCACC CAGCGAGCCG TTGGACGACA ACTGGTACAC CAGAGGATGC CATCCGGCCT

60

(2) INFORMATION FOR SEQ ID NO: 5192:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 320 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5192:

Met Lys Met Ile Asn Lys Leu Ile Val Pro Val Thr Ala Ser Ala Leu
1 5 10 15

EP 0 786 519 A2

	20	25	30
5	Leu Ile Ser Ser Lys Ala Gly Asp Val Thr Val Ala Asp Thr Met Lys 35 40 45		
	Lys Ile Gly Lys Asp Gln Ile Ala Asn Ala Ser Phe Thr Glu Met Leu 50 55 60		
10	Asn Lys Ile Leu Ala Asp Lys Tyr Lys Asn Lys Val Asn Asp Lys Lys 65 70 75 80		
	Ile Asp Glu Gln Ile Glu Lys Met Gln Lys Gln Tyr Gly Gly Lys Asp 85 90 95		
15	Lys Phe Glu Lys Ala Leu Gln Gln Gln Gly Leu Thr Ala Asp Lys Tyr 100 105 110		
	Lys Glu Asn Leu Arg Thr Ala Ala Tyr His Lys Glu Leu Leu Ser Asp 115 120 125		
20	Lys Ile Lys Ile Ser Asp Ser Glu Ile Lys Glu Asp Ser Lys Lys Ala 130 135 140		
	Ser His Ile Leu Ile Lys Val Lys Ser Lys Lys Ser Asp Xaa Glu Gly 145 150 155 160		
25	Leu Asp Asp Lys Glu Ala Lys Gln Lys Ala Glu Glu Ile Gln Lys Glu 165 170 175		
	Val Ser Lys Asp Pro Ser Lys Phe Gly Glu Ile Ala Lys Lys Glu Ser 180 185 190		
30	Met Asp Thr Gly Ser Ala Lys Lys Asp Gly Glu Leu Gly Tyr Val Leu 195 200 205		
	Lys Gly Gln Thr Asp Lys Asp Phe Glu Lys Ala Leu Phe Lys Leu Lys 210 215 220		
35	Asp Gly Glu Val Ser Glu Val Val Lys Ser Ser Phe Gly Tyr His Ile 225 230 235 240		
40	Ile Lys Ala Asp Lys Pro Thr Asp Phe Asn Ser Glu Lys Gln Ser Leu 245 250 255		
	Lys Glu Lys Leu Val Asp Gln Lys Val Gln Lys Asn Pro Lys Leu Leu 260 265 270		
45	Thr Asp Ala Tyr Lys Asp Leu Leu Lys Glu Tyr Asp Val Asp Phe Lys 275 280 285		
	Asp Arg Asp Ile Lys Ser Val Val Glu Asp Lys Ile Leu Asn Pro Glu 290 295 300		
50	Lys Leu Lys Gln Gly Gly Ala Gln Gly Gly Gln Ser Gly Met Ser Gln 305 310 315 320		

55

(2) INFORMATION FOR SEQ ID NO:5193:

(A) LENGTH: 330 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5193:

Met	Asn	Lys	Val	Ile	Lys	Met	Leu	Val	Val	Thr	Leu	Ala	Phe	Leu	Leu	1	5	10	15
Val	Leu	Ala	Gly	Cys	Ser	Gly	Asn	Ser	Asn	Lys	Gln	Ser	Ser	Asp	Asn	20	25	30	
Lys	Asp	Lys	Glu	Thr	Thr	Ser	Ile	Lys	His	Ala	Met	Gly	Thr	Thr	Glu	35	40	45	
Ile	Lys	Gly	Lys	Pro	Lys	Arg	Val	Val	Thr	Leu	Tyr	Gln	Gly	Ala	Thr	50	55	60	
Asp	Val	Ala	Val	Ser	Leu	Gly	Val	Lys	Pro	Val	Gly	Ala	Val	Glu	Ser	65	70	75	80
Trp	Thr	Gln	Lys	Pro	Lys	Phe	Glu	Tyr	Ile	Lys	Asn	Asp	Leu	Lys	Asp	85	90	95	
Thr	Lys	Ile	Val	Gly	Gln	Glu	Pro	Ala	Pro	Asn	Leu	Glu	Glu	Ile	Ser	100	105	110	
Lys	Leu	Lys	Pro	Asp	Leu	Ile	Val	Ala	Ser	Lys	Val	Arg	Asn	Glu	Lys	115	120	125	
Val	Tyr	Asp	Gln	Leu	Ser	Lys	Ile	Ala	Pro	Thr	Val	Ser	Thr	Asp	Thr	130	135	140	
Val	Phe	Lys	Phe	Lys	Asp	Thr	Thr	Lys	Leu	Met	Gly	Lys	Ala	Leu	Gly	145	150	155	160
Lys	Glu	Lys	Glu	Ala	Glu	Asp	Leu	Leu	Lys	Lys	Tyr	Asp	Asp	Lys	Val	165	170	175	
Ala	Ala	Phe	Gln	Lys	Asp	Ala	Lys	Ala	Lys	Tyr	Lys	Asp	Ala	Trp	Pro	180	185	190	
Leu	Lys	Ala	Ser	Val	Val	Asn	Phe	Arg	Ala	Asp	His	Thr	Arg	Ile	Tyr	195	200	205	
Ala	Gly	Gly	Tyr	Ala	Gly	Glu	Ile	Leu	Asn	Asp	Leu	Gly	Phe	Lys	Arg	210	215	220	
Asn	Lys	Asp	Leu	Gln	Lys	Gln	Val	Asp	Asn	Gly	Lys	Asp	Ile	Ile	Gln	225	230	235	240
Leu	Thr	Ser	Lys	Glu	Ser	Ile	Pro	Leu	Met	Asn	Ala	Asp	His	Ile	Phe	245	250	255	

Val Val Lys Ser Asp Pro Asn Ala Lys Asp Ala Ala Leu Val Lys Lys
 260 265 270

5 Thr Glu Ser Glu Trp Thr Ser Ser Lys Glu Trp Lys Asn Leu Asp Ala
 275 280 285

Val Lys Asn Asn Gln Val Ser Asp Asp Leu Asp Glu Ile Thr Trp Asn
 290 295 300

10 Leu Ala Gly Gly Tyr Lys Ser Ser Leu Lys Leu Ile Asp Asp Leu Tyr
 305 310 315 320

Glu Lys Leu Asn Ile Glu Lys Gln Ser Lys
 325 330

(2) INFORMATION FOR SEQ ID NO:5194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5194:

Met Thr Arg Lys Phe Arg Thr Leu Ile Leu Ile Leu Ile Ala Thr Ile
 1 5 10 15

Ala Leu Ser Gly Cys Ala Asn Asp Asp Gly Ile Tyr Ser Asp Lys Gly
 20 25 30

35 Gln Val Phe Arg Lys Ile Leu Ser Ser Asp Leu Thr Ser Leu Asp Thr
 35 40 45

Ser Leu Ile Thr Asp Glu Ile Ser Ser Glu Val Thr Ala Gln Thr Phe
 50 55 60

40 Glu Gly Leu Tyr Thr Leu Gly Lys Gly Asp Lys Pro Val Leu Gly Val
 65 70 75 80

Ala Lys Ala Phe Pro Glu Lys Ser Lys Asp Gly Lys Thr Leu Lys Val
 85 90 95

45 Lys Leu Arg Ser Asp Ala Lys Trp Ser Asn Gly Asp Lys Val Thr Ala
 100 105 110

50 Gln Asp Phe Val Tyr Ala Trp Arg Lys Thr Val Asp Pro Lys Thr Gly
 115 120 125

Ser Glu Phe Ala Tyr Ile Met Gly Asp Ile Lys Asn Ala Ser Asp Ile
 130 135 140

55 Ser Thr Gly Lys Lys Pro Val Glu Gln Leu Gly Ile Lys Ala Leu Asn
 145 150 155 160

EP 0 786 519 A2

Asp Glu Thr Leu Gln Ile Glu Leu Glu Lys Pro Val Pro Tyr Ile Asn
165 170 175
Gln Leu Leu Ala Leu Asn Thr Phe Ala Pro Gln Asn Glu Lys Val Ala
180 185 190
Lys Lys Tyr Gly Lys Asn Tyr Gly Thr Ala Ala Asp Arg Ala Val Tyr
195 200 205
Asn Gly Pro Phe Lys Val Asp Asp Trp Lys Gln Glu Asp Lys Thr Leu
210 215 220
Leu Ser Lys Asn Gln Tyr Tyr Trp Asp Lys Lys Asn Val Lys Leu Asp
225 230 235 240
Lys Val Asn Tyr Lys Val Ile Lys Asp Leu Gln Ala Gly Ala Ser Leu
245 250 255
Tyr Asp Thr Glu Ser Val Asp Asp Ala Phe Ile Thr Ala Asp Gln Val
260 265 270
Asn Lys Tyr Lys Asp Asn Lys Gly Leu Asn Phe Val Leu Thr Thr Gly
275 280 285
Thr Phe Phe Val Lys Met Asn Glu Lys Gln Tyr Pro Asp Phe Lys Asn
290 295 300
Lys Asn Leu Arg Leu Xaa Ser His Lys Gln
305 310

(2) INFORMATION FOR SEQ ID NO:5195:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5195:

Met Lys Arg Leu Ile Gly Leu Val Ile Val Ala Leu Val Leu Leu Ala
1 5 10 15
Ala Cys Gly Gly Asn Asn Asp Lys Lys Val Thr Ile Gly Val Ala Ser
20 25 30
Asn Asp Thr Lys Ala Trp Glu Lys Val Lys Glu Leu Ala Lys Lys Asp
35 40 45
Asp Ile Asp Val Glu Ile Lys His Phe Ser Asp Tyr Asn Leu Pro Asn
50 55 60
Lys Ala Leu Asn Asp Gly Asp Ile Asp Met Asn Ala Phe Gln His Phe
65 70 75 80

Ala Phe Leu Asp Gln Tyr Lys Lys Ala His Lys Gly Thr Lys Ile Ser
85 90 95

5 Ala Leu Ser Thr Thr Val Leu Ala Pro Leu Gly Ile Tyr Ser Asp Lys
100 105 110

Ile Lys Asp Val Lys Lys Val Lys Asp Gly Ala Lys Val Val Ile Pro
115 120 125

10 Asn Asp Val Ser Asn Gln Ala Arg Ala Leu Lys Leu Leu Glu Ala Ala
130 135 140

Gly Leu Ile Lys Leu Lys Lys Asp Phe Gly Leu Ala Gly Thr Val Lys
145 150 155 160

15 Asp Ile Thr Ser Asn Pro Lys His Leu Lys Ile Thr Ala Val Asp Ala
165 170 175

Gln Gln Thr Ala Arg Ala Leu Ser Asp Val Asp Ile Ala Val Ile Asn
180 185 190

20 Asn Gly Val Ala Thr Lys Ala Gly Lys Asp Pro Lys Asn Asp Pro Ile
195 200 205

25 Phe Leu Glu Lys Ser Asn Ser Asp Ala Val Lys Pro Tyr Ile Asn Ile
210 215 220

Val Ala Val Asn Asp Lys Asp Leu Asp Asn Lys Thr Tyr Ala Lys Ile
225 230 235 240

30 Val Glu Leu Tyr His Ser Lys Glu Ala Gln Lys Ala Leu Gln Glu Asp
245 250 255

Val Lys Asp Gly Glu Lys Pro Val Asn Leu Ser Lys Asp Glu Ile Lys
260 265 270

35 Ala Ile Glu Thr Ser Leu Ala Lys
275 280

(2) INFORMATION FOR SEQ ID NO:5196:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5196:

Met Lys Lys Leu Phe Gly Leu Ile Leu Val Leu Thr Phe Ala Val Val
1 5 10 15

55 Leu Ala Ala Cys Gly Asn Gly Asn Lys Ser Gly Ser Asp Asp Lys Lys
20 25 30

EP 0 786 519 A2

Ile Thr Val Ser Ala Ser Pro Ala Pro His Ala Glu Ile Leu Glu Lys
35 40 45

Ala Lys Pro Leu Leu Glu Lys Lys Gly Tyr Glu Leu Asp Ile Lys Thr
5 50 55 60

Ile Asn Asp Tyr Thr Thr Pro Asn Lys Leu Leu Asp Lys Gly Glu Ile
65 70 75 80

Asp Ala Asn Tyr Phe Gln His Thr Pro Tyr Leu Asn Thr Glu Lys Lys
10 85 90 95

Asp Lys Gly Tyr Lys Ile Val Ser Ala Gly Asp Val His Leu Glu Pro
100 105 110

Met Ala Val Tyr Ser Lys Lys Tyr Lys Ser Leu Lys Glu Leu Pro Lys
15 115 120 125

Gly Ala Thr Val Tyr Val Ser Asn Asn Pro Ala Glu Gln Gly Arg Phe
20 130 135 140

Leu Lys Phe Phe Val Asp Ala Gly Leu Ile Lys Ile Lys Lys Gly Val
145 150 155 160

Lys Ile Glu Asp Ala Lys Phe Ser Asp Ile Thr Glu Asn Lys Lys Asp
25 165 170 175

Ile Lys Phe Asn Asn Lys Gln Ser Ala Glu Phe Leu Pro Lys Ile Tyr
180 185 190

Gln Asn Glu Asp Ala Asp Ala Val Ile Ile Asn Ser Asn Phe Ala Ile
30 195 200 205

Glu Gln Lys Leu Asn Pro Lys Lys Asp Ser Ile Ala Val Glu Ser Ala
210 215 220

Lys Asp Asn Pro Tyr Ala Asn Leu Ile Ala Val Lys Glu Gly His Gln
35 225 230 235 240

Asp Asp Lys Lys Ile Lys Ala Leu Ile Glu Val Leu Gln Ser Lys Asp
245 250 255

Ile Gln Asp Phe Ile Asn Glu Lys Tyr Asn Gly Ala Val Ile Pro Ala
40 260 265 270

Lys

(2) INFORMATION FOR SEQ ID NO:5197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5197:

5	Met	Lys	Lys	Ile	Lys	Tyr	Ile	Leu	Val	Val	Phe	Val	Leu	Ser	Leu	Thr	1	5	10	15
	Val	Leu	Ser	Gly	Cys	Ser	Leu	Pro	Gly	Leu	Gly	Ser	Lys	Ser	Thr	Lys	20	25	30	
10	Asn	Asp	Val	Lys	Ile	Thr	Ala	Leu	Ser	Thr	Ser	Glu	Ser	Gln	Ile	Ile	35	40	45	
	Ser	His	Met	Leu	Arg	Leu	Leu	Ile	Glu	His	Asp	Thr	His	Gly	Lys	Ile	50	55	60	
15	Lys	Pro	Thr	Leu	Val	Asn	Asn	Leu	Gly	Ser	Ser	Thr	Ile	Gln	His	Asn	65	70	75	80
	Ala	Leu	Ile	Asn	Gly	Asp	Ala	Asn	Ile	Ser	Gly	Val	Arg	Tyr	Asn	Gly	85	90	95	
20	Thr	Asp	Leu	Thr	Gly	Ala	Leu	Lys	Glu	Ala	Pro	Ile	Lys	Asn	Pro	Lys	100	105	110	
	Lys	Ala	Met	Ile	Ala	Thr	Gln	Gln	Gly	Phe	Lys	Lys	Lys	Phe	Asp	Gln	115	120	125	
25	Thr	Phe	Phe	Asp	Ser	Tyr	Gly	Phe	Ala	Asn	Thr	Tyr	Ala	Phe	Met	Val	130	135	140	
	Thr	Lys	Glu	Thr	Ala	Lys	Lys	Tyr	His	Leu	Glu	Thr	Val	Ser	Asp	Leu	145	150	155	160
30	Ala	Lys	His	Ser	Lys	Asp	Leu	Arg	Leu	Gly	Met	Asp	Ser	Ser	Trp	Met	165	170	175	
	Asn	Arg	Lys	Gly	Asp	Gly	Tyr	Glu	Gly	Phe	Lys	Lys	Glu	Tyr	Gly	Phe	180	185	190	
35	Asp	Phe	Gly	Thr	Val	Arg	Pro	Met	Gln	Ile	Gly	Leu	Val	Tyr	Asp	Ala	195	200	205	
40	Leu	Asn	Ser	Glu	Lys	Leu	Asp	Val	Ala	Leu	Gly	Tyr	Ser	Thr	Asp	Gly	210	215	220	
	Arg	Ile	Ala	Ala	Tyr	Asp	Leu	Lys	Val	Leu	Lys	Asp	Asp	Lys	Gln	Phe	225	230	235	240
45	Phe	Pro	Pro	Tyr	Ala	Ala	Ser	Ala	Val	Ala	Thr	Asn	Glu	Leu	Leu	Arg	245	250	255	
	Gln	His	Pro	Glu	Leu	Lys	Thr	Thr	Ile	Asn	Lys	Leu	Thr	Gly	Lys	Ile	260	265	270	
50	Ser	Thr	Ser	Glu	Met	Gln	Arg	Leu	Asn	Tyr	Glu	Ala	Asp	Gly	Lys	Gly	275	280	285	
55	Lys	Glu	Pro	Ala	Val	Val	Ala	Glu	Glu	Phe	Leu	Lys	Lys	His	His	Tyr	290	295	300	

Phe Asp Lys Gln Lys Gly Gly His Lys
305 310

(2) INFORMATION FOR SEQ ID NO:5198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5198:

Met	Lys	Lys	Leu	Thr	Thr	Leu	Leu	Leu	Ala	Ser	Thr	Leu	Leu	Ile	Ala	1	5	10	15
Ala	Cys	Gly	Asn	Asp	Asp	Ser	Lys	Lys	Asp	Asp	Ser	Lys	Thr	Ser	Lys	20	25	30	
Lys	Asp	Asp	Gly	Val	Lys	Ala	Glu	Leu	Lys	Gln	Ala	Thr	Lys	Ala	Tyr	35	40	45	
Asp	Lys	Tyr	Thr	Asp	Glu	Gln	Leu	Asn	Glu	Phe	Leu	Lys	Gly	Thr	Glu	50	55	60	
Lys	Phe	Val	Lys	Ala	Ile	Glu	Asn	Asn	Asp	Met	Ala	Gln	Ala	Lys	Ala	65	70	75	80
Leu	Tyr	Pro	Lys	Val	Arg	Met	Tyr	Tyr	Glu	Arg	Ser	Glu	Pro	Val	Ala	85	90	95	
Glu	Ala	Phe	Gly	Asp	Leu	Asp	Pro	Lys	Ile	Asp	Ala	Arg	Leu	Ala	Asp	100	105	110	
Met	Lys	Glu	Lys	Lys	Glu	Lys	Glu	Trp	Ser	Gly	Tyr	His	Lys	Ile	115	120	125		
Glu	Lys	Ala	Leu	Tyr	Glu	Asp	Lys	Lys	Ile	Asp	Asp	Val	Thr	Lys	Lys	130	135	140	
Asp	Ala	Gln	Gln	Leu	Leu	Lys	Asp	Ala	Lys	Glu	Leu	His	Ala	Lys	Ala	145	150	155	160
Asp	Thr	Leu	Asp	Ile	Thr	Pro	Lys	Leu	Met	Leu	Gln	Gly	Ser	Val	Asp	165	170	175	
Leu	Leu	Asn	Glu	Val	Ala	Thr	Ser	Lys	Ile	Thr	Gly	Glu	Glu	Glu	Ile	180	185	190	
Tyr	Ser	His	Thr	Asp	Leu	Tyr	Asp	Phe	Lys	Ala	Asn	Val	Glu	Gly	Ala	195	200	205	
Gln	Lys	Ile	Tyr	Asp	Leu	Phe	Lys	Pro	Ile	Leu	Glu	Lys	Lys	Asp	Lys	210	215	220	

EP 0 786 519 A2

Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu
 225 230 235 240
 Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys
 245 250 255
 Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu
 260 265 270
 Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu
 275 280

(2) INFORMATION FOR SEQ ID NO:5199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5199:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala
 1 5 10 15
 Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys
 20 25 30
 Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr
 35 40 45
 Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu
 50 55 60
 Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala
 65 70 75 80
 Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala
 85 90 95
 Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp
 100 105 110
 Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile
 115 120 125
 Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys
 130 135 140
 Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala
 145 150 155 160
 Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp
 165 170 175

Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile
 180 185 190
 Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala
 195 200 205
 Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys
 210 215 220
 Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu
 225 230 235 240
 Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys
 245 250 255
 Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu
 260 265 270
 Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu
 275 280

(2) INFORMATION FOR SEQ ID NO:5200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5200:

Met Lys Phe Lys Ala Ile Val Ala Ile Thr Leu Ser Leu Ser Leu Leu
 1 5 10 15
 Thr Ala Cys Gly Ala Asn Gln His Lys Glu Asn Ser Ser Lys Ser Asn
 20 25 30
 Asp Thr Asn Lys Lys Thr Gln Gln Thr Asp Asn Thr Thr Gln Ser Asn
 35 40 45
 Thr Glu Lys Gln Met Thr Pro Gln Glu Ala Glu Asp Ile Val Arg Asn
 50 55 60
 Asp Tyr Lys Ala Arg Gly Val Asn Glu Tyr Gln Thr Leu Asn Tyr Lys
 65 70 75 80
 Thr Asn Leu Glu Arg Ser Asn Glu His Glu Tyr Tyr Val Glu His Leu
 85 90 95
 Val Arg Asp Ala Val Gly Thr Pro Leu Lys Arg Cys Ala Ile Val Asn
 100 105 110
 Arg His Asn Gly Thr Ile Ile Asn Ile Phe Asp Asp Met Ser Glu Lys
 115 120 125

EP 0 786 519 A2

Asp Lys Glu Glu Phe Glu Ala Phe Lys Lys Arg Ser Pro Lys Tyr Asn
 130 135 140
 Pro Gly Met Asn Asn His Asp Glu Thr Asp Gly Glu Ser Glu Asp Ile
 145 150 155 160
 Gln His His Asp Ile Asp Asn Asn Lys Ala Ile Gln Asn Asp Ile Pro
 165 170 175
 Asp Gln Lys Val Asp Asp Lys Asn Asp Lys Asn Ala Val Asn Lys Glu
 180 185 190
 Glu Lys His Asp Asn Gly Ala Asn Asn Ser Glu Glu Thr Lys Val Lys
 195 200 205

(2) INFORMATION FOR SEQ ID NO:5201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5201:

Met Leu Lys Gly Cys Gly Gly Cys Leu Ile Ser Phe Ile Leu Leu Ile
 1 5 10 15
 Ile Leu Leu Ser Ala Cys Ser Met Met Phe Ser Asn Asn Asp Asn Ser
 20 25 30
 Thr Asn Asn Gln Ser Ser Lys Thr Gln Leu Thr Gln Lys Asp Glu Asn
 35 40 45
 Lys Asn Glu Asp Lys Pro Glu Glu Lys Ser Glu Thr Ala Thr Asp Glu
 50 55 60
 Asp Leu Gln Ser Thr Glu Glu Val Pro Ala Asn Glu Asn Thr Glu Asn
 65 70 75 80
 Asn Gln His Glu Ile Asp Glu Ile Thr Thr Lys Asp Gln Ser Asp Asp
 85 90 95
 Asp Ile Asn Thr Pro Asn Val Ala Glu Asp Lys Ser Gln Asp Asp Leu
 100 105 110
 Lys Asp Asp Leu Lys Glu Lys Gln Gln Ser Ser Asn His His Gln Ser
 115 120 125
 Thr Gln Pro Lys Thr Ser Pro Ser Thr Glu Thr Asn Thr Gln Gln Ser
 130 135 140
 Phe Ala Asn Cys Lys Gln Leu Arg Gln Val Tyr Pro Asn Gly Val Thr

Ala Asp His Pro Ala Tyr Arg Pro His Leu Asp Arg Asp Lys Asp Lys
 165 170 175

Arg Ala Cys Glu Pro Asp Lys Tyr
 180

(2) INFORMATION FOR SEQ ID NO:5202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5202:

Met Lys Lys Arg Leu Leu Leu Ser Thr Phe Leu Ala Ser Thr Leu Ile
 1 5 10 15
 Leu Thr Gly Cys Ala Ser Asp Gln Ser Asp Asn Glu Asp His His Thr
 20 25 30
 Ser Thr Gly Ile His Ala Pro Lys Ser Ala Lys Lys Leu Glu Thr Lys
 35 40 45
 Asp Ile Phe Xaa Ser Asp Lys Lys Asn Ser Asp Ile Ser Asp Ala Glu
 50 55 60
 Met Lys Gln Ala Ile Glu Lys Tyr Leu Ser Val Asn Ser Asp Ile Leu
 65 70 75 80
 Asp Asn Lys Tyr Ile Met Gln His Lys Leu Asp Lys Gln Ile Asp Ser
 85 90 95
 Gln Thr Lys Val Thr Glu Lys Gln Ala Glu Thr Leu Ser His Leu Ser
 100 105 110
 Asn Leu Ala Val Lys Asn Asp Leu His Phe Lys Lys Phe Val Thr Glu
 115 120 125
 Asn Asn Ile Pro Lys Glu Tyr Lys Lys Pro Val Glu Leu Met Met Asn
 130 135 140
 Tyr Phe Lys Ala Leu Asn Ser Thr Ile Ala Asn Val Asp Glu Asp Ile
 145 150 155 160
 Glu Lys Leu Ser Tyr Gln Pro Gln Asn Lys Ile Asn Val Val Asp Val
 165 170 175
 Pro Thr Lys Tyr Ala Gly Asp Val Asn Lys Lys Gln Gln Asp Lys Ile
 180 185 190
 Lys Asp Phe Leu Lys Ser Lys Gly Ile Lys Ser Asp Val Ile Asp Lys

(2) INFORMATION FOR SEQ ID NO:5203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5203:

```

Met Lys Ser Lys Ile Tyr Ile Leu Leu Leu Xaa Leu Ile Phe Leu Ser
 1           5           10           15
Ala Cys Ala Asn Thr Arg His Ser Glu Ser Asp Lys Asn Val Leu Thr
 20           25           30
Val Tyr Ser Pro Tyr Gln Ser Asn Leu Ile Arg Pro Ile Leu Asn Glu
 35           40           45
Xaa Glu Lys Gln Glu His Val Lys Ile Glu Ile Lys His Gly Ser Thr
 50           55           60
Gln Val Leu Leu Ser Asn Leu His Asn Glu Asp Phe Ser Glu Arg Gly
 65           70           75           80
Asp Val Phe Met Gly Gly Val Leu Ser Glu Thr Ile Asp His Pro Glu
 85           90           95
Asp Phe Val Pro Tyr Gln Asp Thr Ser Val Thr Gln Gln Leu Glu Asp
100          105          110
Tyr Arg Ser Asn Asn Lys Tyr Val Thr Ser Phe Leu Leu Met Pro Thr
115          120          125
Val Ile Val Val Asn Ser Asp Leu Gln Gly Asp Ile Lys Ile Arg Gly
130          135          140
Tyr Gln Asp Leu Leu Gln Pro Ile Leu Lys Gly Lys Ile Ala Tyr Ser
145          150          155          160
Asn Pro Asn Thr Thr Thr Thr Gly Tyr Gln His Met Arg Ala Ile Tyr
165          170          175
Ser Met His His Arg Val Ser Asp Val His Gln Phe Gln Asn His Ala
180          185          190
Met Gln Leu Ser Lys Thr Ser Lys Val Ile Glu Asp Val Ala Lys Gly
195          200          205
Lys Tyr Tyr Ala Gly Leu Ser Tyr Glu Gln Asp Ala Arg Thr Trp Lys
210          215          220

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5

10

15

20

25

30

180 185 190
 Phe Tyr Ile Thr Tyr Ser Ser Arg Ser Leu Lys Glu Tyr Arg Lys Tyr
 195 200 205
 5 Tyr Glu Pro Leu Ile Arg Lys Asn Asp Lys Glu Phe Lys Glu Gly Met
 210 215 220
 Glu Arg Ala Arg Lys Glu Val Asn Tyr Ala Ala Asn Thr Asp Ala Val
 225 230 235 240
 10 Ala Thr Leu Phe Ser Thr Lys Lys Asn Phe Thr Lys Asp Asn Thr Val
 245 250 255
 Asp Asp Val Ile Glu Leu Ser Asp Lys Leu Tyr Asn Leu Lys Asn Lys
 260 265 270
 15 Pro Asp Lys Ser Thr Ile Thr Ile Gln Ile Gly Lys Pro Thr Ile Asn
 275 280 285
 20 Thr Lys Lys Ala Phe Tyr Asp Asp Asn Arg Pro Ile Glu Tyr Gly Val
 290 295 300
 His Ser Lys Asp Glu
 305

(2) INFORMATION FOR SEQ ID NO:5205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 193 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5205:

Met Lys Lys Leu Val Ser Ile Val Gly Ala Thr Leu Leu Leu Ala Gly
 1 5 10 15
 Cys Gly Ser Gln Asn Leu Ala Pro Leu Glu Glu Lys Thr Thr Asp Leu
 20 25 30
 45 Arg Glu Asp Asn His Gln Leu Lys Leu Asp Ile Gln Glu Leu Asn Gln
 35 40 45
 Gln Ile Ser Asp Ser Lys Ser Lys Ile Lys Gly Leu Glu Lys Asp Lys
 50 55 60
 50 Glu Asn Ser Lys Lys Thr Ala Ser Asn Asn Thr Lys Ile Lys Leu Met
 65 70 75 80
 Asn Val Thr Ser Thr Tyr Tyr Asp Lys Val Ala Lys Ala Leu Lys Ser
 85 90 95

EP 0 786 519 A2

		100		105		110										
	Val	Gln	Ser	Lys	Leu	Asn	Gln	Ile	Ser	Asn	Asp	Ile	Gln	Ser	Ala	His
			115				120					125				
5	Thr	Ser	Tyr	Lys	Asp	Ala	Ile	Asp	Gly	Leu	Ser	Leu	Ser	Asp	Asp	Asp
		130				135						140				
	Lys	Lys	Thr	Ser	Lys	Asn	Ile	Asp	Lys	Leu	Asn	Ser	Asp	Leu	Asn	His
10		145				150					155				160	
	Ala	Phe	Asp	Asp	Ile	Lys	Asn	Gly	Tyr	Gln	Asn	Lys	Asp	Lys	Lys	Gln
					165					170					175	
	Leu	Thr	Lys	Gly	Gln	Gln	Ala	Leu	Ser	Lys	Leu	Asn	Leu	Asn	Ala	Lys
15				180					185					190		
	Ser															

(2) INFORMATION FOR SEQ ID NO:5206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5206:

35	Met	Lys	Arg	Leu	Leu	Phe	Val	Met	Ile	Ala	Phe	Val	Phe	Ile	Leu	Ala
	1			5						10					15	
	Ala	Cys	Gly	Asn	Asn	Ser	Ser	Lys	Asp	Lys	Glu	Ala	Ser	Lys	Asp	Ser
				20				25						30		
40	Lys	Thr	Ile	Asn	Val	Gly	Thr	Glu	Gly	Thr	Tyr	Ala	Pro	Phe	Ser	Phe
			35				40						45			
	His	Asp	Lys	Asp	Gly	Lys	Leu	Thr	Gly	Tyr	Asp	Ile	Asp	Val	Ile	Lys
		50				55					60					
45	Ala	Val	Ala	Lys	Glu	Glu	Gly	Leu	Lys	Leu	Lys	Phe	Asn	Glu	Thr	Ser
	65				70					75					80	
	Trp	Asp	Ser	Met	Phe	Ala	Gly	Leu	Asp	Ala	Gly	Arg	Phe	Asp	Val	Ile
				85					90					95		
50	Ala	Asn	Gln	Val	Gly	Ile	Asn	Pro	Asp	Arg	Glu	Lys	Lys	Tyr	Lys	Phe
			100					105						110		
	Ser	Lys	Pro	Tyr	Thr	Phe	Ser	Ser	Ala	Val	Leu	Val	Ile	Arg	Glu	Asn
55			115					120					125			

130 135 140
 Gln Thr Phe Thr Ser Asn Tyr Gly Lys Leu Ala Lys Asp Lys Gly Ala
 145 150 155 160
 Asp Ile Thr Lys Val Asp Gly Phe Asn Gln Ser Met Asp Leu Leu Leu
 165 170 175
 Ser Lys Arg Val Asp Gly Thr Phe Asn Asp Ser Leu Ser Tyr Leu Asp
 180 185 190
 Tyr Lys Lys Gln Lys Pro Asn Ala Lys Ile Lys Ala Ile Lys Gly Asn
 195 200 205
 Ala Glu Gln Ser Arg Ser Ala Phe Ala Phe Ser Lys Lys Ala Asp Asp
 210 215 220
 Glu Thr Val Gln Lys Phe Asn Asp Gly Leu Lys Lys Ile Glu Glu Asn
 225 230 235 240
 Gly Glu Leu Ala Lys Ile Gly Lys Lys Trp Phe Gly Gln Asp Val Ser
 245 250 255
 Lys Ser Lys

(2) INFORMATION FOR SEQ ID NO:5207:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5207:

Met Gly Val His Ser Met Lys Leu Lys Arg Leu Phe Ala Val Val Ile
 1 5 10 15
 Ala Met Leu Leu Val Leu Ala Gly Cys Ser Asn Ser Asn Asp Asn Asn
 20 25 30
 Glu Ser Lys Lys Asp Asp Ala Asp Asn Gly Lys Lys Gln Glu Ile Gln
 35 40 45
 Val Ala Ala Ala Ala Ser Leu Thr Asp Val Thr Lys Lys Leu Ala Ser
 50 55 60
 Glu Phe Lys Lys Glu His Lys Asn Ala Asp Ile Lys Phe Asn Tyr Gly
 65 70 75 80
 Gly Ser Gly Ala Leu Arg Lys Gln Ile Glu Ser Gly Ala Pro Val Asp
 85 90 95

100 105 110
 Asn Lys Ala His Asp Thr Tyr Lys Tyr Ala Lys Asn Ser Leu Val Leu
 115 120 125
 Ile Gly Asp Lys Asp Ser Asn Tyr Thr Ser Val Lys Asp Leu Lys Asp
 130 135 140
 Asn Asp Lys Leu Ala Leu Gly Glu Val Lys Thr Val Pro Ala Gly Lys
 145 150 155 160
 Tyr Ala Lys Gln Tyr Leu Asp Asn Asn Asn Leu Phe Lys Glu Val Glu
 165 170 175
 Ser Xaa Ile Val Tyr Ala Lys Asp Val Lys Gln Val Leu Asn Tyr Val
 180 185 190
 Xaa Lys Gly Asn Ala Lys Gln Gly Phe Val Tyr
 195 200

(2) INFORMATION FOR SEQ ID NO:5208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5208:

Met Lys Lys Trp Gln Phe Val Gly Thr Thr Ala Leu Gly Ala Thr Leu
 1 5 10 15
 Leu Leu Gly Ala Cys Gly Gly Gly Asn Gly Gly Ser Gly Asn Ser Asp
 20 25 30
 Leu Lys Gly Glu Ala Lys Gly Asp Gly Ser Ser Thr Val Ala Pro Ile
 35 40 45
 Val Glu Lys Leu Asn Glu Lys Trp Ala Gln Asp His Ser Asp Ala Lys
 50 55 60
 Ile Ser Ala Gly Gln Ala Gly Thr Gly Ala Gly Phe Gln Lys Phe Ile
 65 70 75 80
 Ala Gly Asp Ile Asp Phe Ala Asp Ala Ser Arg Pro Ile Lys Asp Glu
 85 90 95
 Glu Lys Gln Lys Leu Gln Asp Lys Asn Ile Lys Tyr Lys Glu Phe Lys
 100 105 110
 Ile Ala Gln Asp Gly Val Thr Val Ala Val Asn Lys Glu Asn Asp Phe
 115 120 125

	130		135		140													
	Ala	Lys	Thr	Trp	Lys	Asp	Val	Asn	Ser	Lys	Trp	Pro	Asp	Lys	Lys	Ile		
	145					150					155					160		
5	Asn	Ala	Val	Ser	Pro	Asn	Ser	Ser	His	Gly	Thr	Tyr	Asp	Phe	Phe	Glu		
					165					170					175			
	Asn	Glu	Val	Met	Asn	Lys	Glu	Asp	Ile	Lys	Ala	Glu	Lys	Asn	Ala	Asp		
10				180					185					190				
	Thr	Asn	Ala	Ile	Val	Ser	Ser	Val	Thr	Lys	Asn	Lys	Glu	Gly	Ile	Gly		
				195				200					205					
	Tyr	Phe	Gly	Tyr	Asn	Phe	Tyr	Val	Gln	Asn	Lys	Asp	Lys	Leu	Lys	Glu		
15		210					215					220						
	Val	Lys	Ile	Lys	Asp	Glu	Asn	Gly	Lys	Ala	Thr	Glu	Pro	Thr	Lys	Lys		
	225					230				235						240		
	Thr	Ile	Gln	Asp	Asn	Ser	Tyr	Ala	Leu	Ser	Arg	Pro	Leu	Phe	Ile	Tyr		
20					245					250					255			
	Val	Asn	Glu	Lys	Ala	Leu	Lys	Asp	Asn	Lys	Val	Met	Ser	Glu	Phe	Ile		
				260					265					270				
	Lys	Phe	Val	Leu	Glu	Asp	Lys	Gly	Lys	Ala	Ala	Glu	Glu	Ala	Gly	Tyr		
25			275					280					285					
	Val	Ala	Ala	Pro	Glu	Lys	Thr	Tyr	Lys	Ser	Gln	Leu	Asp	Asp	Leu	Lys		
		290					295					300						
	Ala	Phe	Ile	Asp	Lys	Asn	Gln	Lys	Ser	Asp	Asp	Lys	Lys	Ser	Asp	Asp		
30		305				310					315					320		
	Lys	Lys	Ser	Glu	Asp	Lys	Lys											
35					325													

(2) INFORMATION FOR SEQ ID NO:5209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5209:

Met	Lys	Arg	Leu	Ser	Ile	Ile	Val	Ile	Ile	Gly	Ile	Phe	Ile	Ile	Thr
1				5				10					15		
Gly	Cys	Asp	Trp	Gln	Arg	Thr	Ser	Lys	Glu	Arg	Ser	Lys	Asn	Ala	Gln
			20					25					30		

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5210:

```

Met Lys Lys Thr Leu Gly Cys Leu Leu Leu Ile Met Leu Leu Val Val
1           5           10           15
Ala Gly Cys Ser Phe Gly Gly Asn His Lys Leu Ser Ser Lys Lys Ser
15          20          25          30
Glu Glu Ser Lys Gln Glu Thr Val Lys Lys Glu Ser Glu Glu Glu Lys
20          35          40          45
Asp Pro Asp Leu Glu Lys Tyr Glu Glu Ile Glu Lys Lys Met Lys Gly
25          50          55          60
Ile Lys Asp Ala Pro Ser Leu Asp Lys Leu Asp Pro Leu Met Thr Glu
30          65          70          75          80
Lys Ser Phe Thr Asn Ser Lys Gly Ile Gln Gly Trp Lys Asp Tyr Lys
35          85          90          95
Glu Leu Met Gly Lys Val Glu Leu Ala Asp Tyr Arg Phe Thr Lys Asp
40          100         105         110
Ser Lys Gly Ser Ser Ile Lys Asp Val Asp Ala Phe Phe Lys Gly Lys
45          115         120         125
Lys Gly Ile Lys Arg Lys Val Ile Glu Thr His Asp Asp Val Lys Gln
50          130         135         140
Val Asp Tyr Trp
55          145

```

(2) INFORMATION FOR SEQ ID NO:5211:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5211:

```

Trp Pro Cys Ala Thr Xaa Gln Glx Glu Trp Trp Ser Arg His Xaa Trp
1           5           10           15

```

20

25

30

His

5

(2) INFORMATION FOR SEQ ID NO:5212:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 490 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5212:

20

Met Ser Ile Ile Met Glu Val Ala Thr Met Gln Ala Lys Leu Thr Lys
1 5 10 15

Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe Asn
20 25 30

25

Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly
35 40 45

Trp Lys Val Leu Phe Gly Leu Leu Lys Gly Leu Gly Ala Lys Asp
50 55 60

30

Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
65 70 75 80

Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser
85 90 95

35

Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
100 105 110

Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp
115 120 125

40

Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg
130 135 140

45

Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe
145 150 155 160

Lys Ser Glu Thr Ala Pro Arg Ser Val Gln Ser Pro Thr Gln Ala Pro
165 170 175

50

Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile
180 185 190

Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Ser Asn
195 200 205

55

EP 0 786 519 A2

	210	215	220
	Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Leu Ser Arg Leu 225 230 235 240		
5	Glu Ala Gly Ile Ala His Ser Tyr Val Ser Gly Asn Thr Val Trp Gln 245 250 255		
	Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Ile Gly 260 265 270		
10	Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala Asp 275 280 285		
	Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys Ala 290 295 300		
15	Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile Arg 305 310 315 320		
	Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser Val 325 330 335		
20	Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu Asp 340 345 350		
	Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala Tyr 355 360 365		
25	Met Asp Gly Lys Ile Pro Val Ala Thr Val Ser Asn Glu Ser Ser Ala 370 375 380		
	Ser Ser Asn Thr Val Lys Pro Val Ala Ser Ala Trp Lys Arg Asn Lys 385 390 395 400		
30	Tyr Gly Thr Tyr Tyr Met Glu Glu Ser Ala Arg Phe Thr Asn Gly Asn 405 410 415		
	Gln Pro Ile Thr Val Arg Lys Val Gly Pro Phe Leu Ser Cys Pro Val 420 425 430		
35	Gly Tyr Gln Phe Gln Pro Gly Gly Tyr Cys Asp Tyr Thr Glu Val Met 435 440 445		
	Leu Gln Asp Gly His Val Trp Val Gly Tyr Thr Trp Glu Gly Gln Arg 450 455 460		
40	Tyr Tyr Leu Pro Ile Arg Thr Trp Asn Gly Ser Ala Pro Pro Asn Gln 465 470 475 480		
	Ile Leu Gly Asp Leu Trp Gly Glu Ile Ser 485 490		

(2) INFORMATION FOR SEQ ID NO:5213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 299 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5213:

5
 10 Gly Asp Lys Met Asn Lys Ile Ser Lys Tyr Ile Ala Ile Ala Ser Leu
 1 5 10 15
 Ser Val Ala Val Thr Val Ser Ala Pro Gln Thr Thr Asn Ser Thr Ala
 20 25 30
 15 Phe Ala Lys Ser Ser Ala Glu Val Gln Gln Thr Gln Gln Ala Ser Ile
 35 40 45
 Pro Ala Ser Gln Lys Ala Asn Leu Gly Asn Gln Asn Ile Met Ala Val
 50 55 60
 20 Ala Trp Tyr Gln Asn Ser Ala Glu Ala Lys Ala Leu Tyr Leu Gln Gly
 65 70 75 80
 Tyr Asn Ser Ala Lys Thr Gln Leu Asp Lys Glu Ile Lys Lys Asn Lys
 85 90 95
 25 Gly Lys His Lys Leu Ala Ile Ala Leu Asp Leu Asp Glu Thr Val Leu
 100 105 110
 Asp Asn Ser Pro Tyr Gln Gly Tyr Ala Ser Ile His Asn Lys Pro Phe
 115 120 125
 30 Pro Glu Gly Trp His Glu Trp Val Gln Ala Ala Lys Ala Lys Pro Val
 130 135 140
 35 Tyr Gly Ala Lys Glu Phe Leu Lys Tyr Ala Asp Lys Lys Gly Val Asp
 145 150 155 160
 Ile Tyr Tyr Ile Ser Asp Arg Asp Lys Glu Lys Asp Leu Lys Ala Thr
 165 170 175
 40 Gln Lys Asn Leu Lys Gln Gln Gly Ile Pro Gln Ala Lys Lys Ser His
 180 185 190
 Ile Leu Leu Lys Gly Lys Asp Asp Lys Ser Lys Glu Ser Arg Arg Gln
 195 200 205
 45 Met Val Gln Lys Asp His Lys Leu Val Met Leu Phe Gly Asp Asn Leu
 210 215 220
 50 Leu Asp Phe Thr Asp Pro Lys Glu Ala Thr Ala Glu Ser Arg Glu Ala
 225 230 235 240
 Leu Ile Glu Lys His Lys Asp Asp Phe Gly Lys Lys Tyr Ile Ile Phe
 245 250 255
 55 Pro Asn Pro Met Tyr Gly Ser Trp Glu Ala Thr Ile Tyr Asn Asn Asn
 260 265 270

275

280

285

Lys Gln Phe Asp Pro Lys Thr Gly Glu Val Lys
290 295

(2) INFORMATION FOR SEQ ID NO:5214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5214:

Leu Asn Lys Cys Lys Ile Ile Ile Trp Arg Ile Ile Asn Met Lys Asn
1 5 10 15
Lys Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile Gly Ile Thr
20 25 30
Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro
35 40 45
Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn
50 55 60
Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro
65 70 75 80
Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp
85 90 95
Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala
100 105 110
Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln
115 120 125
Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg
130 135 140
Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys
145 150 155 160
Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys Gln Gly Leu
165 170 175
Val Lys

(2) INFORMATION FOR SEQ ID NO:5215:

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5215:

Lys Glu Arg Val Leu Met Lys Lys Leu Leu Thr Ala Ser Ile Ile Ala
 1 5 10 15
 Cys Ser Val Val Met Gly Val Gly Leu Val Asn Thr Ser Ala Glu Ala
 20 25 30
 Ala Ser Gly Asn Ser Ile Asp Thr Val Lys Gln Leu Ile Lys Gly Asp
 35 40 45
 Gln Ser Leu Glu Asn Val Lys Ile Gly Glu Ser Ile Lys Asp Val Leu
 50 55 60
 Thr Lys Tyr Lys Asn Pro Met Tyr Ser Tyr Asn Glu Asp Gly Thr Glu
 65 70 75 80
 His Tyr Tyr Glu Phe His Thr Lys Lys Gly Met Leu Leu Val Thr Thr
 85 90 95
 Asp Gly Lys Lys Asn Asn Gly Lys Val Thr His Ile Ser Met Met Tyr
 100 105 110
 Asn Asp Ala Asn Gly Pro Thr Tyr Gln Ala Val Lys Asn Tyr Val Gly
 115 120 125
 Lys Ala Val Thr His Thr Glu Tyr Ser Lys Val Ala Gly Asn Phe Gly
 130 135 140
 Tyr Ile Glu Lys Gly Lys Thr Thr Tyr Gln Phe Ala Ser Ala Pro Lys
 145 150 155 160
 Asp Lys Asn Ile Lys Leu Tyr Arg Ile Asp Leu Glu Lys
 165 170

(2) INFORMATION FOR SEQ ID NO:5216:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5216:

1 5 10 15

Asn Glu Asp Gly Ser Lys Lys Lys Met Ser Thr Thr Ala Lys Val Val
20 25 30

5 Ser Ile Ala Thr Val Leu Leu Leu Leu Gly Gly Leu Val Phe Ala Ile
35 40 45

10 Phe Ala Tyr Val Asp His Ser Asn Lys Ala Lys Glu Arg Met Leu Asn
50 55 60

Glu Gln Lys Gln Glu Gln Lys Glu Lys Arg Gln Lys Glu Asn Ala Glu
65 70 75 80

15 Lys Glu Arg Lys Lys Lys Gln Gln Glu Glu Lys Glu Gln Asn Glu Leu
85 90 95

Asp Ser Gln Ala Asn Gln Tyr Gln Gln Leu Pro Gln Gln Asn Gln Tyr
100 105 110

20 Gln Tyr Val Pro Pro Gln Gln Gln Ala Pro Thr Lys Gln Arg Pro Ala
115 120 125

Lys Glu Glu Asn Asp Asp Lys Ala Ser Lys Asp Glu Ser Lys Asp Lys
130 135 140

25 Asp Asp Lys Ala Ser Gln Asp Lys Ser Asp Asp Asn Gln Lys Lys Thr
145 150 155 160

30 Asp Asp Asn Lys Gln Pro Ala
165

(2) INFORMATION FOR SEQ ID NO:5217:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5217:

45 Met Lys Arg Asn Phe Pro Lys Leu Ile Ala Leu Ser Leu Ile Phe Ser
1 5 10 15

Leu Ser Val Thr Pro Ile Ala Asn Ala Glu Ser Asn Ser Asn Ile Lys
20 25 30

50 Ala Lys Asp Lys Lys His Val Gln Val Asn Val Glu Asp Lys Ser Val
35 40 45

55 Pro Thr Asp Val Arg Asn Leu Ala Gln Lys Asp Tyr Leu Ser Tyr Val
50 55 60

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5219:

Ile Glu Ser Arg Phe Ile Met Ala Lys Ile Asn Phe Asp Ala Ala Thr
 1 5 10 15
 Lys Gly Asn Pro Gly Ile Ser Thr Cys Ala Ile Val Ile Lys Glu Asp
 20 25 30
 Glu Gln His Tyr Thr Tyr Thr His Glu Leu Gly Glu Met Asp Asn His
 35 40 45
 Thr Ala Glu Trp Ala Ala Cys Ile Tyr Ala Leu Glu His Ala Arg Glu
 50 55 60
 Leu Asn Val Gln Asn Ala Leu Leu Tyr Thr Asp Ser Lys Leu Ile Ala
 65 70 75 80
 Asp Ser Ile Glu Ala Gly Tyr Val Lys Asn Ala Asn Phe Lys Pro Tyr
 85 90 95
 Phe Asp Gln Ile Glu Ile Phe Glu Lys Asp Phe Asp Leu Leu Phe Val
 100 105 110
 Lys Trp Ile Pro Arg Glu Gln Asn Lys Glu Ala Asn Gln His Ala Gln
 115 120 125
 Gln Ala Leu Tyr Lys Leu Ile Lys Lys Asn Lys
 130 135

(2) INFORMATION FOR SEQ ID NO:5220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5220:

Met Pro Gly Thr Val Leu Asp Pro Gln Met Ile Lys Asn Glu Asp Val
 1 5 10 15

EP 0 786 519 A2

[illegible]

(2) INFORMATION FOR SEQ ID NO:5221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5221:

Ile	Met	Ala	Tyr	Asp	Gly	Leu	Phe	Thr	Lys	Lys	Met	Val	Glu	Ser	Leu
1				5					10					15	
Gln	Phe	Leu	Thr	Thr	Gly	Arg	Val	His	Lys	Ile	Asn	Gln	Pro	Asp	Asn
			20					25					30		
Asp	Thr	Ile	Leu	Met	Val	Val	Arg	Gln	Asn	Arg	Gln	Asn	His	Gln	Leu
		35					40					45			
Leu	Leu	Ser	Ile	His	Pro	Asn	Phe	Ser	Arg	Leu	Gln	Leu	Thr	Thr	Lys
	50					55					60				
Lys	Tyr	Asp	Asn	Pro	Phe	Asn	Pro	Pro	Met	Phe	Ala	Arg	Val	Phe	Arg
65					70					75					80

EP 0 786 519 A2

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Asp Arg Arg Ile Glu Ile Asp Ile Lys Ser Lys Asp Glu Ile Gly Asp
100 105 110

Thr Ile Tyr Arg Thr Val Ile Leu Glu Ile Met Gly Lys His Ser Asn
115 120 125

10

Leu Ile Leu Val Asp Glu Asn Arg Lys Ile Ile Glu Gly Phe Lys His
130 135 140

Leu Thr Pro Asn Thr Asn His Tyr Arg Thr Val Met Pro Gly Phe Asn
145 150 155 160

15

Tyr Glu Ala Pro Pro Thr Gln His Lys Ile Asn Pro Tyr Asp Ile Thr
165 170 175

Gly Ala Glu Val Leu Lys Tyr Ile Asp Phe Asn Ala Gly Asn Ile Ala
180 185 190

20

Lys Gln Leu Leu Asn Gln Phe Glu Gly Phe Ser Pro Leu Ile Thr Asn
195 200 205

Glu Ile Val Ser Arg Arg Gln Phe Met Thr Ser Ser Thr Leu Pro Glu
210 215 220

25

Ala Phe Asp Glu Val Met Ala Glu Thr Lys Leu Pro Pro Thr Pro Ile
225 230 235 240

30

Phe His Lys Asn His Glu Thr Gly Lys Glu Asp Phe Tyr Phe Ile Lys
245 250 255

Leu Asn Gln Phe Asn Asp Asp Thr Val Thr Tyr Asp Ser Leu Asn Asp
260 265 270

35

Leu Leu Asp Arg Phe Tyr Asp Ala Arg Gly Glu Arg Glu Arg Val Lys
275 280 285

Gln Arg Ala Asn Asp Leu Val Arg Phe Val Gln Gln Gln Leu His Lys
290 295 300

40

Tyr Gln Asn Lys Leu Ala Ser
305 310

(2) INFORMATION FOR SEQ ID NO:5222:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5222:

EP 0 786 519 A2

	1		5		10		15									
	Glu	Gln	Leu	Tyr	Gly	Glu	Leu	Ile	Thr	Ala	Asn	Ile	Tyr	Arg	Ile	Lys
5				20				25					30			
	Gln	Gly	Asp	Lys	Glu	Val	Thr	Ala	Leu	Asn	Tyr	Tyr	Thr	Asn	Glu	Glu
			35					40					45			
10	Val	Val	Ile	Pro	Leu	Asn	Pro	Thr	Lys	Ser	Pro	Ser	Ala	Asn	Ala	Gln
	50					55						60				
	Tyr	Tyr	Tyr	Lys	Gln	Tyr	Xaa	Arg	Met	Lys	Thr	Arg	Xaa	Arg	Glu	Leu
	65					70					75				80	
15	Gln	His	Gln	Ile	Gln	Leu	Thr	Lys	Asp	Asn	Ile	Asp	Tyr	Phe	Ser	Thr
					85					90					95	
	Ile	Glu	Gln	Gln	Leu	His	His	Ile	Ser	Val	His	Asp	Ile	Asp	Glu	Ile
20					100				105					110		
	Arg	Asp	Glu	Leu	Ala	Glu	Gln	Gly	Phe	Met	Lys	Gln	Arg	Lys	Asn	Gln
			115					120					125			
25	Thr	Lys	Lys	Lys	Lys	Ala	Gln	Ile	Gln	Leu	Gln	His	Tyr	Val	Ser	Thr
		130					135					140				
	Asp	Gly	Asp	Asp	Ile	Tyr	Val	Gly	Lys	Asn	Asn	Lys	Gln	Asn	Asp	Tyr
	145					150					155				160	
30	Leu	Thr	Asn	Lys	Lys	Ala	Lys	Lys	Thr	His	Thr	Trp	Leu	His	Thr	Lys
					165					170					175	
	Asp	Ile	Pro	Gly	Ser	His	Val	Val	Ile	Phe	Asn	Asp	Ala	Pro	Ser	Asp
35				180					185					190		
	Thr	Thr	Ile	Lys	Glu	Ala	Ala	Met	Leu	Ala	Gly	Tyr	Phe	Ser	Lys	Ala
			195					200					205			
40	Gly	Asn	Ser	Gly	Gln	Ile	Pro	Val	Asp	Tyr	Thr	Leu	Ile	Lys	Asn	Val
		210					215					220				
	His	Lys	Pro	Ser	Gly	Ala	Lys	Pro	Gly	Phe	Val	Thr	Tyr	Asp	Asn	Gln
	225					230					235					240
45	Lys	Thr	Leu	Tyr	Ala											
					245											

(2) INFORMATION FOR SEQ ID NO:5223:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 99 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5223:

Tyr Ile Thr Asn Pro Gln Asn Pro Lys Ile Lys Ile Thr Gly Ile Ser
 1 5 10 15
 Leu Ser Ser Gly Val Gly Asn Phe Phe Ile Ile Thr Asn Gly Lys Arg
 20 25 30
 Ile Ile Val Ala Lys Ile Lys Arg Asn Ala Asp Asn Asp Ser Ala Leu
 35 40 45
 Lys Ser Phe Asn Ala Ile Phe Ile Ile Gly Asn Ala Asp Pro His Asn
 50 55 60
 Met Ile Val Asn Lys Tyr Asp Arg Lys Val Val Ser Arg Ser Leu Phe
 65 70 75 80
 Ile Asn Ile Ile Thr Pro Leu Ile Met Cys Phe Tyr Ile Lys Lys Tyr
 85 90 95
 Asp Leu Lys

(2) INFORMATION FOR SEQ ID NO:5224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5224:

Glu Asn Val Leu Ala Lys Glu Tyr Ala Val Lys Tyr Asn Ala Val Glu
 1 5 10 15
 Ala Ile Gln His Arg Gly Glu Thr Val Thr Glu Gly Ser Ser Ser Asn
 20 25 30
 Ala Tyr Ala Ile Lys Asp Gly Val Ile Tyr Thr His Pro Ile Asn Asn
 35 40 45
 Tyr Ile Leu Asn Gly Ile Thr Arg Ile Val Ile Lys Lys Ile Ala Glu
 50 55 60
 Asp Tyr Asn Ile Pro Phe Lys Glu Glu Thr Phe Thr Val Asp Phe Leu
 65 70 75 80
 Lys Asn Ala Asp Glu Val Ile Val Ser Ser Thr Ser Ala Glu Val Thr
 85 90 95
 Pro Val Ile Lys Leu Asp Gly Glu Pro Val Asn Asp Gly Lys Val Gly
 100 105 110

115

120

125

His Ser Ile
130

(2) INFORMATION FOR SEQ ID NO:5225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5225:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn
1 5 10 15
Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile
20 25 30
Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr
35 40 45
Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala
50 55 60
Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln
65 70 75 80
Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro
85 90 95
Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly
100 105 110
Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp
115 120 125
Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala
130 135 140
Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala
145 150 155 160
Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln
165 170 175
Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala
180 185 190
Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp
195 200 205

EP 0 786 519 A2

	210	215	220
5	Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly 225 230 235 240		
	Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn 245 250 255		
10	Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val 260 265 270		
	Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys 275 280 285		
15	Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr 290 295 300		
	Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp 305 310 315 320		
20	Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly 325 330 335		
	Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu 340 345 350		
25	Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr 355 360 365		
	Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly 370 375 380		
30	Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro 385 390 395 400		
	Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn 405 410 415		
35	Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu 420 425 430		
40	Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr 435 440 445		
	Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr 450 455 460		
45	Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly 465 470 475 480		
	Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp 485 490 495		
50	Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr 500 505 510		
55	Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser 515 520 525		

530

535

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(2) INFORMATION FOR SEQ ID NO:5226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5226:

Tyr Lys Glu Leu Ser His Gly Arg Leu Ile Gly Gly Thr Lys Met His
 1 5 10 15
 Lys Lys Tyr Phe Ile Gly Thr Ser Ile Leu Ile Ala Val Phe Val Val
 20 25 30
 Ile Phe Asp Gln Val Thr Lys Tyr Ile Ile Ala Thr Thr Met Lys Ile
 35 40 45
 Gly Asp Ser Phe Glu Val Ile Pro His Phe Leu Asn Ile Thr Ser His
 50 55 60
 Arg Asn Asn Gly Ala Ala Trp Gly Ile Leu Ser Gly Lys Met Thr Phe
 65 70 75 80
 Phe Phe Ile Ile Thr Ile Ile Ile Leu Ile Ala Leu Val Tyr Phe Phe
 85 90 95
 Ile Lys Asp Ala Gln Tyr Asn Leu Phe Met Gln Val Ala Ile Ser Leu
 100 105 110
 Leu Phe Ala Gly Ala Leu Gly Asn Phe Ile Asp Arg Ile Leu Thr Gly
 115 120 125
 Glu Val Val Asp Phe Ile Asp Thr Asn Ile Phe Gly Tyr Asp Phe Pro
 130 135 140
 Ile Phe Asn Ile Ala Asp Ser Ser Leu Thr Ile Gly Val Ile Leu Ile
 145 150 155 160
 Ile Ile Ala Leu Leu Lys Asp Thr Ser Asn Lys Lys Glu Lys Glu Val
 165 170 175
 Lys

(2) INFORMATION FOR SEQ ID NO:5227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5227:

Ala Gly Lys Ser Ser Leu Ile Lys Ser Leu Ile Gly Glu Phe Asn Ala
1 5 10 15

Thr Gly Thr Lys Leu Leu Tyr Asn Lys Pro Ile Gln Gln Gln Leu Gln
20 25 30

His Ile Thr Tyr Ile Pro Gln Lys Ala His Ile Asp Leu Asp Phe Pro
35 40 45

Ile Ser Val Glu Gln Val Ile Leu Ser Gly Cys Tyr Lys Glu Ile Gly
50 55 60

Trp Phe Arg Arg Pro Asn Lys Ser Ala Arg Asp Lys Leu Lys Gln Leu
65 70 75 80

Leu Ser Asp Leu Glu Leu Glu Ser Leu Arg His Arg Gln Ile Ser Glu
85 90 95

Leu Ser Gly Gly Gln Leu Gln Arg Val Leu Val Ala Arg Ala Leu Met
100 105 110

Ser Xaa Ser Glu Val Tyr Phe Leu Asp Glu Pro Phe Val Gly Ile Asp
115 120 125

Phe Ser Ser Glu Lys Leu Ile Met Thr Lys Ile Glu Asn Leu Lys Gln
130 135 140

Gln Gly Lys Leu Ile Leu Ile Ile His His Asp Leu Ser Lys Ala Lys
145 150 155 160

Gln Tyr Phe Asp Arg Ile Ile Leu Leu Asn Gln Thr Leu Arg Tyr Phe
165 170 175

Gly Asp Ser Glu Glu Ala Met Ser Val Thr Arg Leu Asn Glu Thr Phe
180 185 190

Met Ser Ser Thr Asp Cys Ser Asp Pro Ser Gln Arg Ser Asn Ile Thr
195 200 205

Cys

45

(2) INFORMATION FOR SEQ ID NO:5228:

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 256 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5228:

5 Thr Phe Arg Ile Ile Phe Leu Leu Ser Ile Arg Lys Arg Ser Asn Arg
 1 5 10 15
 Thr His Val Ser Ile His Trp Ser Thr Val Asn Lys Glu Glu Ile Cys
 20 25 30
 10 Leu Arg Val Lys Asp Asn Leu Gln Gln Ile Ser Thr Gln Ile Asn Asp
 35 40 45
 Lys Ser Glu Lys Asn Asn Phe Ser Thr Lys Pro Asn Val Ile Ala Val
 50 55 60
 15 Thr Lys Tyr Val Thr Ile Glu Arg Ala Lys Glu Ala Tyr Glu Ala Gly
 65 70 75 80
 Ile Arg His Phe Gly Glu Asn Arg Leu Glu Gly Phe Phe Gln Lys Lys
 85 90 95
 20 Glu Ala Leu Pro Ser Asp Ala Val Ile His Phe Ile Gly Ser Leu Gln
 100 105 110
 Ser Arg Lys Val Lys Asp Val Ile Asn Asp Val Asp Tyr Phe His Ala
 115 120 125
 25 Leu Asp Arg Leu Ser Leu Ala Lys Glu Ile Asn Lys Arg Ala Glu His
 130 135 140
 30 Lys Ile Lys Cys Phe Leu Gln Val Asn Val Ser Gly Glu Ala Ser Lys
 145 150 155 160
 His Gly Ile Ala Leu Glu Asp Val Asp Gln Phe Ile Asp Asp Leu Lys
 165 170 175
 35 Lys Tyr Asp Lys Ile Glu Ile Val Gly Leu Met Thr Met Ala Pro Leu
 180 185 190
 Thr Asp Asp Glu Ala Tyr Ile Arg Ser Leu Phe Lys Gln Leu Arg Leu
 195 200 205
 40 Lys Lys Glu Glu Ile Gln Arg Leu Asn Leu Glu Tyr Ala Pro Cys Asp
 210 215 220
 45 Glu Leu Ser Met Gly Met Ser Asn Asp Tyr Leu Ile Ala Val Glu Glu
 225 230 235 240
 Gly Ala Thr Phe Val Arg Ile Gly Thr Lys Leu Val Gly Glu Glu Glu
 245 250 255

(2) INFORMATION FOR SEQ ID NO:5229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5229:

10 Lys His Lys Leu Thr Ile Ile Thr Gly Gly Phe Phe Thr Met Lys Lys
 1 5 10 15
 Thr Ile Met Ala Ser Ser Leu Ala Val Ala Leu Gly Val Thr Gly Tyr
 20 25 30
 15 Ala Ala Gly Thr Gly His Gln Ala His Ala Ala Glu Val Asn Val Asp
 35 40 45
 Gln Ala His Leu Val Asp Leu Ala His Asn His Gln Asp Gln Leu Asn
 50 55 60
 20 Ala Ala Pro Ile Lys Asp Gly Ala Tyr Asp Ile His Phe Val Lys Asp
 65 70 75 80
 Gly Phe Gln Tyr Asn Phe Thr Ser Asn Gly Thr Thr Trp Ser Trp Ser
 85 90 95
 25 Tyr Glu Ala Ala Asn Gly Gln Thr Ala Gly Phe Ser Asn Val Ala Gly
 100 105 110
 Ala Asp Tyr Thr Thr Ser Tyr Asn Gln Gly Ser Asn Val Gln Ser Val
 115 120 125
 Ser Tyr Asn Ala Gln Ser Ser Asn Ser Asn Val Glu Ala Val Ser Ala
 130 135 140
 35 Pro Thr Tyr His Asn Tyr Ser Thr Ser Thr Thr Ser Ser Ser Val Arg
 145 150 155 160
 Leu Ser Asn Gly Asn Thr Ala Gly Ala Thr Gly Ser Ser Ala Ala Gln
 165 170 175
 40 Ile Met Ala Gln Arg Thr Gly Val Ser Ala Ser Thr Trp Ala Ala Ile
 180 185 190
 Ile Ala Arg Glu Ser Asn Gly Gln Val Asn Ala Tyr Asn Pro Ser Gly
 195 200 205
 45 Ala Ser Gly Leu Phe Gln Thr Met Pro Gly Trp Gly Pro Thr Asn Thr
 210 215 220
 Val Asp Gln Gln Ile Asn Ala Ala Val Lys Ala Tyr Lys Ala Gln Gly
 225 230 235 240
 50 Leu Gly Ala Trp Gly Phe
 245

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(2) INFORMATION FOR SEQ ID NO:5230:

(A) LENGTH: 519 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5230:

Lys	Glu	Pro	His	Lys	Met	Lys	Lys	Ile	Tyr	Lys	Ser	Leu	Thr	Val	Ser	1	5	10	15
Ala	Ile	Val	Ala	Thr	Val	Ser	Leu	Ser	Ala	Leu	Pro	Gln	Ser	Leu	Ala	20	25	30	
Ile	Thr	His	Glu	Ser	Gln	Pro	Thr	Lys	Gln	Gln	Arg	Thr	Val	Leu	Phe	35	40	45	
Asp	Arg	Ser	His	Gly	Gln	Thr	Ala	Gly	Ala	Ala	Asp	Trp	Val	Ser	Asp	50	55	60	
Gly	Ala	Phe	Ser	Asp	Tyr	Ala	Asp	Ser	Ile	Gln	Lys	Gln	Gly	Tyr	Asp	65	70	75	80
Val	Lys	Ala	Ile	Asp	Gly	His	Ser	Asn	Ile	Thr	Glu	Ala	Ser	Leu	Lys	85	90	95	
Ser	Ser	Lys	Ile	Phe	Val	Ile	Pro	Glu	Ala	Asn	Ile	Pro	Phe	Lys	Glu	100	105	110	
Ser	Glu	Gln	Ala	Ala	Ile	Val	Lys	Tyr	Val	Lys	Gln	Gly	Gly	Asn	Val	115	120	125	
Val	Phe	Ile	Ser	Asp	His	Tyr	Asn	Ala	Asp	Arg	Asn	Leu	Asn	Arg	Ile	130	135	140	
Asp	Ser	Ser	Glu	Ala	Met	Asn	Gly	Tyr	Arg	Arg	Gly	Ala	Tyr	Glu	Asp	145	150	155	160
Met	Ser	Lys	Gly	Met	Asn	Ala	Glu	Glu	Lys	Ser	Ser	Thr	Ala	Met	Gln	165	170	175	
Gly	Val	Lys	Ser	Ser	Asp	Trp	Leu	Ser	Thr	Asn	Phe	Gly	Val	Arg	Phe	180	185	190	
Arg	Tyr	Asn	Ala	Leu	Gly	Asp	Leu	Asn	Thr	Ser	Asn	Ile	Val	Ser	Ser	195	200	205	
Lys	Glu	Ser	Phe	Gly	Ile	Thr	Glu	Gly	Val	Lys	Ser	Val	Ser	Met	His	210	215	220	
Ala	Gly	Ser	Thr	Leu	Ala	Ile	Thr	Asn	Pro	Glu	Lys	Ala	Lys	Gly	Ile	225	230	235	240
Val	Tyr	Thr	Pro	Glu	Gln	Leu	Pro	Ala	Lys	Ser	Lys	Trp	Ser	His	Ala	245	250	255	

Val Asp Gln Gly Ile Tyr Asn Gly Gly Gly Lys Ala Glu Gly Pro Tyr
 260 265 270
 Val Ala Ile Ser Lys Val Gly Lys Gly Lys Ala Ala Phe Ile Gly Asp
 275 280 285
 Ser Ser Leu Val Glu Asp Ser Ser Pro Lys Tyr Val Arg Glu Asp Asn
 290 295 300
 Gly Glu Lys Lys Lys Thr Tyr Asp Gly Phe Lys Glu Gln Asp Asn Gly
 305 310 315 320
 Lys Leu Leu Asn Asn Ile Thr Ala Trp Met Ser Lys Asp Asn Asp Gly
 325 330 335
 Lys Ser Leu Lys Ala Ser Ser Leu Thr Leu Asp Thr Lys Thr Lys Leu
 340 345 350
 Leu Asp Phe Glu Arg Pro Glu Arg Ser Thr Glu Pro Glu Lys Glu Pro
 355 360 365
 Trp Ser Gln Pro Pro Ser Gly Tyr Lys Trp Tyr Asp Pro Thr Thr Phe
 370 375 380
 Lys Ala Gly Ser Tyr Gly Ser Glu Lys Gly Ala Asp Pro Gln Pro Asn
 385 390 395 400
 Thr Pro Asp Asp His Thr Pro Pro Asn Gln Asn Glu Lys Val Thr Phe
 405 410 415
 Asp Ile Pro Gln Asn Val Ser Val Asn Glu Pro Phe Glu Met Thr Ile
 420 425 430
 His Leu Lys Gly Phe Glu Ala Asn Gln Thr Leu Glu Asn Leu Arg Val
 435 440 445
 Gly Ile Tyr Lys Glu Gly Gly Arg Gln Ile Gly Gln Phe Ser Ser Lys
 450 455 460
 Asp Asn Asp Tyr Asn Pro Pro Gly Tyr Ser Thr Leu Pro Thr Val Lys
 465 470 475 480
 Ala Asp Glu Asn Gly Asn Val Thr Ile Lys Val Asn Ala Lys Val Leu
 485 490 495
 Glu Ser Met Glu Gly Ser Lys Ile Arg Leu Lys Leu Gly Asp Lys Thr
 500 505 510
 Leu Ile Thr Thr Asp Phe Lys
 515

(2) INFORMATION FOR SEQ ID NO:5231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5231:

5	Arg	Asp	Glu	Arg	Ile	Lys	Thr	Met	Thr	Asn	Ser	Ser	Lys	Ser	Phe	Thr	1	5	10	15
	Lys	Phe	Met	Ala	Ala	Ser	Ala	Val	Phe	Thr	Met	Gly	Phe	Leu	Ser	Val	20	25	30	
10	Pro	Thr	Ala	Gly	Ala	Glu	Gln	Thr	Asn	Gln	Ile	Ala	Asn	Lys	Pro	Gln	35	40	45	
	Ala	Ile	Gln	Trp	His	Thr	Asn	Leu	Thr	Asn	Glu	Arg	Phe	Thr	Thr	Ile	50	55	60	
15	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Ala	Pro	Glu	His	Thr	Phe	Gln	Ala	65	70	75	80
	Tyr	Asp	Lys	Ser	His	Asn	Glu	Leu	Lys	Ala	Ser	Tyr	Ile	Glu	Ile	Asp	85	90	95	
20	Leu	Gln	Arg	Thr	Lys	Asp	Gly	His	Leu	Val	Ala	Met	His	Asp	Glu	Thr	100	105	110	
	Val	Asn	Arg	Thr	Thr	Asn	Gly	His	Gly	Lys	Val	Glu	Asp	Tyr	Thr	Leu	115	120	125	
25	Asp	Glu	Leu	Lys	Gln	Leu	Asp	Ala	Gly	Ser	Trp	Phe	Asn	Lys	Lys	Tyr	130	135	140	
30	Pro	Lys	Tyr	Ala	Arg	Ala	Ser	Tyr	Lys	Asn	Ala	Lys	Val	Pro	Thr	Leu	145	150	155	160
	Asp	Glu	Ile	Leu	Glu	Arg	Tyr	Gly	Pro	Asn	Ala	Asn	Tyr	Tyr	Ile	Glu	165	170	175	
35	Thr	Lys	Ser	Pro	Asp	Val	Tyr	Pro	Gly	Met	Glu	Glu	Gln	Leu	Leu	Ala	180	185	190	
40	Ser	Leu	Lys	Lys	His	His	Leu	Leu	Asn	Asn	Asn	Lys	Leu	Lys	Asn	Gly	195	200	205	
	His	Val	Met	Ile	Gln	Ser	Phe	Ser	Asp	Glu	Ser	Leu	Lys	Lys	Ile	His	210	215	220	
45	Arg	Gln	Asn	Lys	His	Val	Pro	Leu	Val	Lys	Leu	Val	Asp	Lys	Gly	Glu	225	230	235	240
	Leu	Gln	Gln	Phe	Asn	Asp	Gln	Arg	Leu	Lys	Glu	Ile	Arg	Ser	Tyr	Ala	245	250	255	
50	Ile	Gly	Leu	Gly	Pro	Asp	Tyr	Thr	Asp	Leu	Thr	Glu	Gln	Asn	Thr	His	260	265	270	
55	His	Leu	Lys	Asp	Leu	Gly	Phe	Ile	Val	His	Pro	Tyr	Thr	Val	Asn	Glu	275	280	285	

Lys Ala Asp Met Leu Arg Leu Asn Lys Tyr Gly Val Asp Gly Val Phe
 290 295 300

Thr Asn Phe Ala Asp Lys Tyr Lys Glu Val Ile Lys
 305 310 315

(2) INFORMATION FOR SEQ ID NO:5232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5232:

Arg Phe Met Lys Asn Leu Ile Ser Ile Ile Ile Ile Leu Cys Leu Thr
 1 5 10 15

Leu Ser Ile Met Thr Pro Tyr Ala Gln Ala Thr Asn Ser Asp Val Thr
 20 25 30

Pro Val Gln Ala Ala Asn Gln Tyr Gly Tyr Ala Gly Leu Ser Ala Ala
 35 40 45

Tyr Glu Pro Thr Ser Ala Val Asn Val Ser Gln Thr Gly Gln Leu Leu
 50 55 60

Tyr Gln Tyr Asn Ile Asp Thr Lys Trp Asn Pro Ala Ser Met Thr Lys
 65 70 75 80

Leu Met Thr Met Tyr Leu Thr Leu Glu Ala Val Asn Lys Gly Gln Leu
 85 90 95

Ser Leu Asp Asp Thr Val Thr Met Thr Asn Lys Glu Tyr Ile Met Ser
 100 105 110

Thr Leu Pro Glu Leu Ser Asn Thr Lys Leu Tyr Pro Gly Gln Val Trp
 115 120 125

Thr Ile Ala Asp Leu Leu Gln Ile Thr Val Ser Asn Ser Ser Asn Ala
 130 135 140

Ala Ala Leu Ile Leu Ala Lys Lys Val Ser Lys Asn Thr Ser Asp Phe
 145 150 155 160

Val Asp Leu Met Asn Asn Lys Ala Lys Ala Ile Gly Met Lys Asn Thr
 165 170 175

His Phe Val Asn Pro Thr Gly Ala Glu Asn Ser Arg Leu Arg Thr Phe
 180 185 190

Ala Pro Thr Lys Tyr Lys Asp Gln Glu Arg Thr Val Thr Thr Ala Arg
 195 200 205

EP 0 786 519 A2

Asp Tyr Ala Ile Leu Asp Leu His Val Ile Lys Glu Thr Pro Lys Ile
 210 215 220
 5 Leu Asp Phe Thr Lys Gln Leu Ala Pro Thr Thr His Ala Val Thr Tyr
 225 230 235 240
 Tyr Thr Phe Asn Phe Ser Leu Glu Gly Ala Lys Met Ser Leu Pro Gly
 245 250 255
 10 Thr Asp Gly Leu Lys Thr Gly Ser Ser Asp Thr Ala Asn Tyr Asn His
 260 265 270
 Thr Ile Thr Thr Lys Arg Gly Lys Phe Arg Ile Asn Gln Val Ile Met
 275 280 285
 15 Gly Ala Gly Asp Tyr Lys Asn Leu Gly Gly Glu Lys Gln Arg Asn Met
 290 295 300
 Met Gly Asn Ala Leu Met Glu Arg Ser Phe Asp Gln Tyr Lys Tyr Val
 305 310 315 320
 20 Lys Ile Leu Ser Lys Gly Glu Gln Arg Ile Asn Gly Lys Lys Tyr Tyr
 325 330 335
 Val Glu Asn Asp Leu Tyr Asp Val Leu Pro Ser Asp Phe Ser Lys Lys
 340 345 350
 25 Asp Tyr Lys Leu Val Val Glu Asp Gly Lys Val His Ala Asp Tyr Pro
 355 360 365
 30 Arg Glu Phe Ile Asn Lys Asp Tyr Gly Pro Pro Thr Val Glu Val His
 370 375 380
 Gln Pro Ile Ile Gln Lys Ala Asn Thr Val Ala Lys Ser Met Trp Glu
 385 390 395 400
 35 Glu His Pro Leu Phe Thr Ile Ile Gly Gly Thr Cys Leu Val Ala Gly
 405 410 415
 Leu Ala Leu Ile Val His Met Ile Ile Asn Arg Leu Phe Arg Lys Arg
 420 425 430
 40 Lys

(2) INFORMATION FOR SEQ ID NO:5233:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 50 (ii) MOLECULE TYPE: protein
 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5233:

Leu Thr Lys Glu Arg Glu Tyr Met Lys Leu Lys Ser Phe Ile Thr Val
 1 5 10 15
 Thr Leu Ala Leu Gly Met Ile Ala Thr Thr Gly Ala Thr Val Ala Gly
 20 25 30
 Asn Glu Val Ser Ala Ala Glu Lys Asp Lys Leu Pro Ala Thr Gln Lys
 35 40 45
 Ala Lys Glu Met Gln Asn Val Pro Tyr Thr Ile Ala Val Asp Gly Ile
 50 55 60
 Met Ala Phe Asn Gln Ser Tyr Leu Asn Leu Pro Lys Asp Ser Gln Leu
 65 70 75 80
 Ser Tyr Leu Asp Leu Gly Asn Lys Val Lys Ala Leu Leu Tyr Asp Glu
 85 90 95
 Arg Gly Val Thr Pro Glu Lys Ile Arg Asn Ala Lys Ser Ala Val Tyr
 100 105 110
 Thr Ile Thr Trp Lys Asp Gly Ser Lys Lys Glu Val Asp Leu Lys Lys
 115 120 125
 Asp Ser Tyr Thr Ala Asn Leu Phe Asp Ser Asn Ser Ile Lys Gln Ile
 130 135 140
 Asp Ile Asn Val Lys Thr Lys
 145 150

(2) INFORMATION FOR SEQ ID NO:5234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5234:

Asn His Cys Asn Arg Ile Glu Arg Lys Met Ala Met Ser Asn Asn Phe
 1 5 10 15
 Lys Asp Asp Phe Glu Lys Asn Arg Gln Ser Ile Asp Thr Asn Ser His
 20 25 30
 Gln Asp His Thr Glu Asp Val Glu Lys Asp Gln Ser Glu Leu Glu His
 35 40 45
 Gln Asp Thr Ile Glu Asn Thr Glu Gln Gln Phe Pro Pro Arg Asn Ala
 50 55 60
 Gln Arg Arg Lys Arg Arg Arg Asp Leu Ala Thr Asn His Asn Lys Gln
 65 70 75 80

EP 0 786 519 A2

	Val	His	Asn	Glu	Ser	Gln	Thr	Ser	Glu	Asp	Asn	Val	Gln	Asn	Glu	Ala
					85					90					95	
5	Gly	Thr	Ile	Asp	Asp	Arg	Gln	Val	Glu	Ser	Ser	His	Ser	Thr	Glu	Ser
				100					105					110		
	Gln	Glu	Pro	Ser	His	Gln	Asp	Ser	Thr	Pro	Gln	His	Glu	Glu	Glu	Tyr
			115					120					125			
10	Tyr	Asn	Lys	Asn	Ala	Phe	Ala	Met	Asp	Lys	Ser	His	Pro	Glu	Pro	Ile
		130					135					140				
	Glu	Asp	Asn	Asp	Lys	His	Asp	Thr	Ile	Lys	Asn	Ala	Glu	Asn	Asn	Thr
	145					150					155					160
15	Glu	His	Ser	Thr	Val	Ser	Asp	Lys	Ser	Glu	Ala	Glu	Gln	Ser	Gln	Gln
					165					170					175	
	Pro	Lys	Pro	Tyr	Phe	Thr	Thr	Gly	Ala	Asn	Gln	Ser	Glu	Thr	Ser	Lys
20				180					185					190		
	Asn	Glu	His	Asp	Asn	Asp	Ser	Val	Lys	Gln	Asp	Gln	Asp	Glu	Pro	Lys
			195					200					205			
	Glu	His	His	Asn	Gly	Lys	Lys	Ala	Ala	Ala	Ile	Gly	Ala	Gly	Thr	Ala
25		210					215					220				
	Gly	Val	Ala	Gly	Ala	Ala	Gly	Ala	Met	Ala	Ala	Ser	Lys	Ala	Lys	Lys
	225					230					235					240
30	His	Ser	Asn	Asp	Ala	Gln	Asn	Lys	Ser	Asn	Ser	Gly	Lys	Ala	Asn	Asn
					245					250					255	
	Ser	Thr	Glu	Asp	Lys	Ala	Ser	Gln	Asp	Lys	Ser	Lys	Asp	His	His	Asn
				260					265					270		
35	Gly	Lys	Lys	Gly	Ala	Ala	Ile	Gly	Ala	Gly	Thr	Ala	Gly	Leu	Ala	Gly
			275					280					285			
	Gly	Ala	Ala	Ser	Lys	Ser	Ala	Ser	Ala	Ala	Ser	Lys	Pro	His	Ala	Ser
		290					295					300				
40	Asn	Asn	Ala	Ser	Gln	Asn	His	Asp	Glu	His	Asp	Asn	His	Asp	Arg	Asp
	305					310					315					320
	Lys	Glu	Arg	Lys	Lys	Gly	Gly	Met	Ala	Lys	Val	Leu	Leu	Pro	Leu	Ile
45					325					330					335	
	Ala	Ala	Val	Leu	Ile	Ile	Gly	Ala	Leu	Ala	Ile	Phe	Gly	Gly	Met	Ala
				340					345					350		
	Leu	Asn	Asn	His	Asn	Asn	Gly	Thr	Lys	Glu	Asn	Lys	Ile	Ala	Asn	Thr
50			355					360					365			
	Asn	Lys	Asn	Asn	Ala	Asp	Glu	Ser	Lys	Asp	Lys	Asp	Thr	Ser	Lys	Asp
		370					375					380				
55	Ala	Ser	Lys	Asp	Lys	Ser	Lys	Ser	Thr	Asp	Ser	Asp	Lys	Ser	Lys	Glu
	385					390					395					400

Asp Gln Asp Lys Ala Thr Lys Asp Glu Ser Asp Asn Asp Gln Asn Asn
 405 410 415
 Ala Asn Gln Ala Asn Asn Gln Ala Gln Asn Asn Gln Asn Gln Gln Gln
 420 425 430
 Ala Asn Gln Asn Gln Gln Gln Gln Gln Arg Gln Gly Gly Gly Gln
 435 440 445
 Arg His Thr Val Asn Gly Gln Glu Asn Leu Tyr Arg Ile Ala Ile Gln
 450 455 460
 Tyr Tyr Gly Ser Gly Ser Pro Glu Asn Val Glu Lys Ile Arg Arg Ala
 465 470 475 480
 Asn Gly Leu Ser Gly Asn Asn Ile Arg Asn Gly Gln Gln Ile Val Ile
 485 490 495
 Pro

(2) INFORMATION FOR SEQ ID NO:5235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 886 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5235:

Leu Leu Ser Ile Lys Tyr Asn Leu Ile Gly Val Val Asn Asn Met Asn
 1 5 10 15
 Lys His His Pro Lys Leu Arg Ser Phe Tyr Ser Ile Arg Lys Ser Thr
 20 25 30
 Leu Gly Val Ala Ser Val Ile Val Ser Thr Leu Phe Leu Ile Thr Ser
 35 40 45
 Gln His Gln Ala Gln Ala Ala Glu Asn Thr Asn Thr Ser Asp Lys Ile
 50 55 60
 Ser Glu Asn Gln Asn Asn Asn Ala Thr Thr Thr Gln Pro Pro Lys Asp
 65 70 75 80
 Thr Asn Gln Thr Gln Pro Ala Thr Gln Pro Ala Asn Thr Ala Lys Asn
 85 90 95
 Tyr Pro Ala Ala Asp Glu Ser Leu Lys Asp Ala Ile Lys Asp Pro Ala
 100 105 110
 Leu Glu Asn Lys Glu His Asp Ile Gly Pro Arg Glu Gln Val Asn Phe
 115 120 125

10

NSDOCID: <EP__0788519A2_1_>

EP 0 786 519 A2

	Val	Lys	Ile	Val	Ser	Ser	Ile	Glu	Tyr	Gly	Glu	Asn	Ile	His	Glu	Asp	
	450						455					460					
5	Tyr	Asp	Tyr	Thr	Leu	Met	Val	Phe	Ala	Gln	Pro	Ile	Thr	Asn	Asn	Pro	
	465					470					475					480	
	Asp	Asp	Tyr	Val	Asp	Glu	Glu	Thr	Tyr	Asn	Leu	Gln	Lys	Leu	Leu	Ala	
					485					490					495		
10	Pro	Tyr	His	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Glu	
				500					505					510			
	Lys	Leu	Gln	Glu	Lys	Leu	Pro	Glu	Lys	Tyr	Lys	Ala	Glu	Tyr	Lys	Lys	
			515					520					525				
15	Lys	Leu	Asp	Gln	Thr	Arg	Val	Glu	Leu	Ala	Asp	Gln	Val	Lys	Ser	Ala	
	530						535					540					
	Val	Thr	Glu	Phe	Glu	Asn	Val	Thr	Pro	Thr	Asn	Asp	Gln	Leu	Thr	Asp	
	545					550					555					560	
20	Leu	Gln	Glu	Ala	His	Phe	Val	Val	Phe	Glu	Ser	Glu	Glu	Asn	Ser	Glu	
					565					570					575		
	Ser	Val	Met	Asp	Gly	Phe	Val	Glu	His	Pro	Phe	Tyr	Thr	Ala	Thr	Leu	
25				580					585					590			
	Asn	Gly	Gln	Lys	Tyr	Val	Val	Met	Lys	Thr	Lys	Asp	Asp	Ser	Tyr	Trp	
			595					600					605				
30	Lys	Asp	Leu	Ile	Val	Glu	Gly	Lys	Arg	Val	Thr	Thr	Val	Ser	Lys	Asp	
	610						615					620					
	Pro	Lys	Asn	Asn	Ser	Arg	Thr	Leu	Ile	Phe	Pro	Tyr	Ile	Pro	Asp	Lys	
	625					630					635					640	
35	Ala	Val	Tyr	Asn	Ala	Ile	Val	Lys	Val	Val	Val	Ala	Asn	Ile	Gly	Tyr	
					645					650					655		
	Glu	Gly	Gln	Tyr	His	Val	Arg	Ile	Ile	Asn	Gln	Asp	Ile	Asn	Thr	Lys	
				660					665					670			
40	Asp	Asp	Asp	Thr	Ser	Gln	Asn	Asn	Thr	Ser	Glu	Pro	Leu	Asn	Val	Gln	
			675					680					685				
	Thr	Gly	Gln	Glu	Gly	Lys	Val	Ala	Asp	Thr	Asp	Val	Ala	Glu	Asn	Ser	
	690					695						700					
45	Ser	Thr	Ala	Thr	Asn	Pro	Lys	Asp	Ala	Ser	Asp	Lys	Ala	Asp	Val	Ile	
	705					710					715					720	
	Glu	Pro	Glu	Ser	Asp	Val	Val	Lys	Asp	Ala	Asp	Asn	Asn	Ile	Asp	Lys	
50					725					730					735		
	Asp	Val	Gln	His	Asp	Val	Asp	His	Leu	Ser	Asp	Met	Ser	Asp	Asn	Asn	
				740					745					750			
55	His	Phe	Asp	Lys	Tyr	Asp	Leu	Lys	Glu	Met	Asp	Thr	Gln	Ile	Ala	Lys	
			755					760					765				

Asp Thr Asp Arg Asn Val Asp Lys Asp Ala Asp Asn Ser Val Gly Met
 770 775 780
 Ser Ser Asn Val Asp Thr Asp Lys Asp Ser Asn Lys Asn Lys Asp Lys
 785 790 795 800
 Val Ile Gln Leu Asn His Ile Ala Asp Lys Asn Asn His Thr Gly Lys
 805 810 815
 Ala Ala Lys Leu Asp Val Val Lys Gln Asn Tyr Asn Asn Thr Asp Lys
 820 825 830
 Val Thr Asp Lys Lys Thr Thr Glu His Leu Pro Ser Asp Ile His Lys
 835 840 845
 Thr Val Asp Lys Thr Val Lys Thr Lys Glu Lys Ala Gly Thr Pro Ser
 850 855 860
 Lys Glu Asn Lys Leu Ser Gln Ser Lys Met Leu Thr Lys Asn Trp Arg
 865 870 875 880
 Asn Asn Xaa Gln Ala Asn
 885

(2) INFORMATION FOR SEQ ID NO:5236:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 236 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5236:

Asn Met Asn Lys Asn Val Met Val Lys Gly Leu Thr Ala Leu Thr Ile
 1 5 10 15
 Leu Thr Ser Leu Gly Phe Ala Glu Asn Ile Ser Asn Gln Xaa His Ser
 20 25 30
 Ile Ala Lys Ala Glu Lys Asn Val Lys Glu Ile Thr Asp Ala Thr Lys
 35 40 45
 Glu Pro Tyr Asn Ser Val Val Ala Phe Val Gly Gly Thr Gly Val Val
 50 55 60
 Val Gly Lys Asn Thr Ile Val Thr Asn Lys His Ile Ala Lys Ser Asn
 65 70 75 80
 Asp Ile Phe Lys Asn Arg Val Ser Ala His His Ser Ser Lys Gly Lys
 85 90 95
 Gly Gly Gly Asn Tyr Asp Val Lys Asp Ile Val Glu Tyr Pro Gly Lys
 100 105 110

Glu Asp Leu Ala Ile Val His Val His Glu Thr Ser Thr Glu Gly Leu
 115 120 125
 Asn Phe Asn Lys Asn Val Ser Tyr Thr Lys Phe Ala Asp Gly Ala Lys
 130 135 140
 Val Lys Asp Arg Ile Ser Val Ile Gly Tyr Pro Lys Gly Ala Gln Thr
 145 150 155 160
 Lys Tyr Lys Met Phe Glu Ser Thr Gly Thr Ile Asn His Ile Ser Gly
 165 170 175
 Thr Phe Met Glu Phe Asp Ala Tyr Ala Gln Pro Gly Asn Ser Gly Ser
 180 185 190
 Pro Val Leu Asn Ser Lys His Xaa Leu Ile Gly Ile Leu Tyr Ala Gly
 195 200 205
 Ser Gly Lys Asp Glu Ser Glu Lys Asn Phe Gly Val Tyr Phe Thr Pro
 210 215 220
 Gln Leu Xaa Xaa Phe Ile Pro Asn Asn Ile Glu Lys
 225 230 235

(2) INFORMATION FOR SEQ ID NO:5237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5237:

Tyr Arg Leu Glu His Thr Ile Met Lys Met Arg Thr Ile Ala Lys Thr
 1 5 10 15
 Ser Leu Ala Leu Gly Leu Leu Thr Thr Gly Ala Ile Thr Val Thr Thr
 20 25 30
 Gln Ser Val Lys Ala Glu Lys Ile Gln Ser Thr Lys Val Asp Lys Val
 35 40 45
 Pro Thr Leu Lys Ala Glu Arg Leu Ala Met Ile Asn Ile Thr Ala Gly
 50 55 60
 Ala Asn Ser Ala Thr Thr Gln Ala Ala Asn Thr Arg Gln Glu Arg Thr
 65 70 75 80
 Pro Lys Leu Glu Lys Ala Pro Asn Thr Asn Glu Glu Lys Thr Ser Ala
 85 90 95
 Ser Lys Ile Glu Lys Ile Ser Gln Pro Lys Gln Glu Glu Gln Lys Thr
 100 105 110

Leu Asn Ile Ser Ala Thr Pro Ala Pro Lys Gln Glu Gln Ser Gln Thr
 115 120 125
 5 Thr Thr Glu Ser Thr Thr Pro Lys Thr Lys Val Thr Thr Pro Pro Ser
 130 135 140
 Thr Asn Thr Pro Gln Pro Met Gln Ser Thr Lys Ser Asp Thr Pro Gln
 145 150 155 160
 10 Ser Pro Thr Ile Lys Gln Ala Gln Thr Asp Met Thr Pro Lys Tyr Glu
 165 170 175
 Asp Leu Arg Ala Tyr Tyr Thr Lys Pro Ser Phe Glu Phe Glu Lys Gln
 180 185 190
 15 Phe Gly Phe Met Leu Lys Pro Trp Thr Thr Val Arg Phe Met Asn Val
 195 200 205
 Ile Pro Asn Arg Phe Ile Tyr Lys Ile Ala Leu Val Gly Lys Asp Glu
 210 215 220
 20 Lys Lys Tyr Lys Asp Gly Pro Tyr Asp Asn Ile Asp Val Phe Ile Val
 225 230 235 240
 Leu Glu Asp Asn Lys Tyr Gln Leu Lys Lys Tyr Ser Val Gly Gly Ile
 245 250 255
 25 Thr Lys Thr Asn Ser Lys Lys Val Asn His Lys Val Glu Leu Ser Ile
 260 265 270
 30 Thr Lys Lys Asp Asn Gln Gly Met Ile Ser Arg Asp Val Ser Glu Tyr
 275 280 285
 Met Ile Thr Lys Glu Glu Ile Ser Leu Lys Glu Leu Asp Phe Lys Leu
 290 295 300
 35 Arg Lys Gln Leu Ile Glu Lys His Asn Leu Tyr Gly Asn Met Gly Ser
 305 310 315 320
 Gly Thr Ile Val Ile Lys Met Lys Asn Gly Gly Lys Tyr Thr Phe Glu
 325 330 335
 40 Leu His Lys Lys Leu Gln Glu His Arg Met Ala Asp Val Ile Asp Gly
 340 345 350
 45 Thr Asn Ile Asp Asn Ile Glu Val Asn Ile Lys
 355 360

(2) INFORMATION FOR SEQ ID NO:5238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5238:

5 Phe Met Lys Phe Lys Ser Leu Ile Thr Thr Thr Leu Ala Leu Gly Val
 1 5 10 15
 Leu Ala Ser Thr Gly Ala Asn Phe Asn Asn Asn Glu Ala Ser Ala Ala
 20 25 30
 10 Ala Lys Pro Leu Asp Lys Ser Ser Ser Ser Leu His His Gly Tyr Ser
 35 40 45
 Lys Val His Val Pro Tyr Ala Ile Thr Val Asn Gly Thr Ser Gln Asn
 50 55 60
 15 Ile Leu Ser Ser Leu Thr Phe Asn Lys Asn Gln Asn Ile Ser Tyr Lys
 65 70 75 80
 Asp Leu Glu Asp Arg Val Lys Ser Val Leu Lys Ser Asp Arg Gly Ile
 85 90 95
 20 Ser Asp Ile Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Tyr
 100 105 110
 Phe Lys Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ala Gly Ile Tyr
 115 120 125
 25 Thr Ala Asp Leu Ile Asn Thr Ser Glu Ile Lys Ala Ile Asn Ile Asn
 130 135 140
 Val Asp Thr Lys Lys Gln
 145 150
 30

(2) INFORMATION FOR SEQ ID NO:5239:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 239 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5239:

45 Glu Lys Arg Phe Met Gln Met Ala Arg Lys Val Val Val Val Asp Asp
 1 5 10 15
 Glu Lys Pro Ile Ala Asp Ile Leu Glu Phe Asn Leu Lys Lys Glu Gly
 20 25 30
 50 Tyr Asp Val Tyr Cys Ala Tyr Asp Gly Asn Asp Ala Val Asp Leu Ile
 35 40 45
 Tyr Glu Glu Glu Pro Asp Ile Val Leu Leu Asp Ile Met Leu Pro Gly
 50 55 60
 55

Arg Asp Gly Met Glu Val Cys Arg Glu Val Arg Lys Lys Tyr Glu Met
 65 70 75 80
 5 Pro Ile Ile Met Leu Thr Ala Lys Asp Ser Glu Ile Asp Lys Val Leu
 85 90 95
 Gly Leu Glu Leu Gly Ala Asp Asp Tyr Val Thr Lys Pro Phe Ser Thr
 100 105 110
 10 Arg Glu Leu Ile Ala Arg Val Lys Ala Asn Leu Arg Arg His Tyr Ser
 115 120 125
 Gln Pro Ala Gln Asp Thr Gly Asn Val Thr Asn Glu Ile Thr Ile Lys
 130 135 140
 15 Asp Ile Val Ile Tyr Pro Asp Ala Tyr Ser Ile Lys Lys Arg Gly Glu
 145 150 155 160
 Asp Ile Glu Leu Thr His Arg Glu Phe Glu Leu Phe His Tyr Leu Ser
 165 170 175
 20 Lys His Met Gly Gln Val Met Thr Arg Glu His Leu Leu Gln Thr Val
 180 185 190
 Trp Gly Tyr Asp Tyr Phe Gly Asp Val Arg Thr Val Asp Val Thr Ile
 195 200 205
 25 Arg Arg Leu Arg Glu Lys Ile Glu Asp Asp Pro Ser His Pro Glu Tyr
 210 215 220
 Ile Val Thr Arg Arg Gly Val Gly Tyr Phe Leu Gln Gln His Glu
 225 230 235
 30

(2) INFORMATION FOR SEQ ID NO:5240:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 133 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 35

(ii) MOLECULE TYPE: protein
 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5240:

Xaa Leu Ser Thr Val Ile Gly Ala Xaa Leu Phe Phe Lys Ser Ser Val
 1 5 10 15
 Ser Leu Val Phe Lys Met Val Lys Lys Phe Arg Xaa Gly Val Ile Ser
 20 25 30
 50 Val Asn Asp Val Met Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys
 35 40 45
 Asn Ala Phe Ser Leu Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val
 50 55 60
 55

Ser Val Leu Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu
 65 70 75 80

Ile Lys Tyr Thr Ala Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys
 85 90 95

Ala Asn Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe
 100 105 110

Tyr Asn Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu
 115 120 125

Phe Asp Val Lys Ala
 130

(2) INFORMATION FOR SEQ ID NO:5241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 508 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:

Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val
 1 5 10 15

Asn Val Arg Asp Tyr Ile Ala Glu Asn Tyr Gly Leu Phe Ile Asn Gly
 20 25 30

Glu Phe Val Lys Gly Ser Ser Asp Glu Thr Ile Glu Val Thr Asn Pro
 35 40 45

Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp
 50 55 60

Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser
 65 70 75 80

Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp
 85 90 95

Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn
 100 105 110

Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala
 115 120 125

Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly
 130 135 140

Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu
 145 150 155 160

EP 0 786 519 A2

Pro Ile Gly Val Val Gly Ala Val Val Ala Trp Asn Phe Pro Met Leu
165 170 175

5 Leu Ala Ala Trp Lys Ile Ala Pro Ala Ile Ala Ala Gly Asn Thr Ile
180 185 190

Val Ile Gln Pro Ser Ser Ser Thr Pro Leu Ser Leu Leu Glu Val Ala
195 200 205

10 Lys Ile Phe Gln Glu Val Leu Pro Lys Gly Val Val Asn Ile Leu Thr
210 215 220

Gly Lys Gly Ser Glu Ser Gly Asn Ala Ile Phe Asn His Asp Gly Val
225 230 235 240

15 Asp Lys Leu Ser Phe Thr Gly Ser Thr Asp Val Gly Tyr Gln Val Ala
245 250 255

Glu Ala Ala Ala Lys His Leu Val Pro Ala Thr Leu Glu Leu Gly Gly
260 265 270

20 Lys Ser Ala Asn Ile Ile Leu Asp Asp Ala Asn Leu Asp Leu Ala Val
275 280 285

Glu Gly Ile Gln Leu Gly Ile Leu Phe Asn Gln Gly Glu Val Cys Ser
290 295 300

25 Ala Gly Ser Arg Leu Leu Val His Glu Lys Ile Tyr Asp Gln Leu Val
305 310 315 320

Pro Arg Leu Gln Glu Ala Phe Ser Asn Ile Lys Val Gly Asn Pro Gln
325 330 335

30 Asp Glu Ala Thr Gln Met Gly Ser Gln Thr Gly Lys Asp Gln Leu Asp
340 345 350

35 Lys Ile Gln Ser Tyr Ile Asp Ala Ala Lys Glu Ser Asp Ala Gln Ile
355 360 365

Leu Ala Gly Gly His Arg Leu Thr Glu Asn Gly Leu Asp Lys Gly Phe
370 375 380

40 Phe Phe Glu Pro Thr Leu Ile Ala Val Pro Asp Asn His His Lys Leu
385 390 395 400

Ala Gln Glu Glu Ile Phe Gly Pro Val Leu Thr Val Ile Lys Val Lys
405 410 415

45 Asp Asp Gln Glu Ala Ile Asp Ile Ala Asn Asp Ser Glu Tyr Gly Leu
420 425 430

Ala Gly Gly Val Phe Ser Gln Asn Ile Thr Arg Ala Leu Asn Ile Ala
435 440 445

50 Lys Ala Val Arg Thr Gly Arg Ile Trp Ile Asn Thr Tyr Asn Gln Val
450 455 460

Pro Glu Gly Ala Pro Phe Gly Gly Tyr Lys Lys Ser Gly Ile Gly Arg
465 470 475 480

Glu Thr Tyr Lys Gly Ala Leu Ser Asn Tyr Gln Gln Val Lys Asn Ile
 485 490 495

Tyr Ile Asp Thr Ser Asn Ala Leu Lys Gly Leu Tyr
 500 505

(2) INFORMATION FOR SEQ ID NO:5242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5242:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn
 1 5 10 15
 Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile
 20 25 30
 Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr
 35 40 45
 Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala
 50 55 60
 Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln
 65 70 75 80
 Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro
 85 90 95
 Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly
 100 105 110
 Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp
 115 120 125
 Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala
 130 135 140
 Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala
 145 150 155 160
 Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln
 165 170 175
 Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala
 180 185 190
 Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp
 195 200 205

EP 0 786 519 A2

	Pro	Ala	Ile	Ser	Thr	Asp	Glu	Asn	Arg	Gln	Asp	Pro	Thr	Val	Thr	Val	
	210						215					220					
5	Thr	Asp	Lys	Val	Asn	Gly	Tyr	Ser	Leu	Ile	Asn	Asn	Gly	Lys	Ile	Gly	
	225					230					235					240	
	Phe	Val	Asn	Ser	Glu	Leu	Arg	Arg	Ser	Asp	Met	Phe	Asp	Lys	Asn	Asn	
					245					250					255		
10	Pro	Gln	Asn	Tyr	Gln	Ala	Lys	Gly	Asn	Val	Ala	Ala	Leu	Gly	Arg	Val	
				260					265					270			
	Asn	Ala	Asn	Asp	Ser	Thr	Asp	His	Gly	Asn	Phe	Asn	Gly	Ile	Ser	Lys	
			275					280					285				
15	Thr	Val	Asn	Val	Lys	Pro	Asp	Ser	Glu	Leu	Ile	Ile	Asn	Phe	Thr	Thr	
	290						295					300					
	Met	Gln	Thr	Asn	Ser	Lys	Gln	Gly	Ala	Thr	Asn	Leu	Val	Ile	Lys	Asp	
	305					310					315					320	
20	Ala	Lys	Lys	Asn	Thr	Glu	Leu	Ala	Thr	Val	Asn	Val	Ala	Lys	Thr	Gly	
					325					330					335		
	Thr	Ala	His	Leu	Phe	Lys	Val	Pro	Thr	Asp	Ala	Asp	Arg	Leu	Asp	Leu	
25				340					345					350			
	Gln	Phe	Ile	Pro	Asp	Asn	Thr	Ala	Val	Ala	Asp	Ala	Ser	Arg	Ile	Thr	
			355					360					365				
30	Thr	Asn	Lys	Asp	Gly	Tyr	Lys	Tyr	Tyr	Ser	Phe	Ile	Asp	Asn	Val	Gly	
	370					375						380					
	Leu	Phe	Ser	Gly	Ser	His	Leu	Tyr	Val	Lys	Asn	Arg	Asp	Leu	Ala	Pro	
	385					390					395					400	
35	Lys	Ala	Thr	Asn	Asn	Lys	Glu	Tyr	Thr	Ile	Asn	Thr	Glu	Ile	Gly	Asn	
					405					410					415		
	Asn	Gly	Asn	Phe	Gly	Ala	Ser	Leu	Lys	Ala	Asp	Gln	Phe	Lys	Tyr	Glu	
				420					425					430			
40	Val	Thr	Leu	Pro	Gln	Gly	Val	Thr	Tyr	Val	Asn	Asn	Ser	Leu	Thr	Thr	
			435					440					445				
	Thr	Phe	Pro	Asn	Gly	Asn	Glu	Asp	Ser	Thr	Val	Leu	Lys	Asn	Met	Thr	
	450					455						460					
45	Val	Asn	Tyr	Asp	Gln	Asn	Ala	Asn	Lys	Val	Thr	Phe	Thr	Ser	Gln	Gly	
	465					470					475					480	
	Val	Thr	Thr	Ala	Arg	Gly	Thr	His	Thr	Lys	Glu	Val	Leu	Phe	Pro	Asp	
				485						490					495		
50	Lys	Ser	Leu	Lys	Leu	Ser	Tyr	Lys	Val	Asn	Val	Ala	Asn	Ile	Asp	Thr	
			500						505					510			
55	Pro	Lys	Asn	Ile	Asp	Phe	Asn	Glu	Lys	Leu	Thr	Tyr	Arg	Thr	Ala	Ser	
	515							520					525				

Asp Val Val Ile Asn Asn Ala Gln Pro Glu Val His
 530 535 540

(2) INFORMATION FOR SEQ ID NO:5243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5243:

Ile Thr Leu Lys Thr Val Ser Gln Leu Ile Asp Met Lys Gln Lys Gln
 1 5 10 15
 Thr Lys Ile Ser Met Val Thr Ala Tyr Asp Phe Pro Ser Ala Lys Gln
 20 25 30
 Val Glu Ala Ala Gly Ile Asp Met Ile Leu Val Gly Asp Ser Leu Gly
 25 35 40 45
 Met Thr Val Leu Gly Tyr Glu Ser Thr Val Gln Val Thr Leu Ala Asp
 50 55 60
 Met Ile His His Gly Arg Ala Val Arg Arg Gly Ala Pro Asn Thr Phe
 30 65 70 75 80
 Val Val Val Asp Met Pro Ile Gly Ala Val Gly Ile Ser Met Thr Gln
 85 90 95
 Asp Leu Asn His Ala Leu Lys Leu Tyr Gln Glu Thr Asn Ala Asn Ala
 35 100 105 110
 Ile Lys Ala Glu Gly Ala His Ile Thr Pro Phe Ile Glu Lys Ala Thr
 115 120 125
 Ala Ile Gly Ile Pro Val Val Ala His Leu Gly Leu Thr Pro Gln Ser
 40 130 135 140
 Val Gly Val Met Gly Tyr Lys Leu Gln Gly Ala Thr Lys Glu Ala Ala
 145 150 155 160
 Glu Gln Leu Ile Leu Asp Ala Lys Asn Val Glu Gln Ala Gly Ala Val
 45 165 170 175
 Ala Leu Val Leu Glu Ala Ile Pro Asn Asp Leu Ala Glu Glu Ile Ser
 180 185 190
 Lys His Leu Thr Ile Pro Val Ile Gly Ile Gly Ala Gly Lys Gly Thr
 195 200 205
 Asp Gly Gln Val Leu Val Tyr His Asp Met Leu Asn Tyr Gly Val Glu
 55 210 215 220

EP 0 786 519 A2

His Lys Ala Lys Phe Val Lys Gln Phe Ala Asp Phe Ser Val Gly Val
 225 230 235 240
 Asp Gly Leu Lys Gln Tyr Asp Gln Glu Val Lys Ser Gly Ala Phe Pro
 245 250 255
 Ser Glu Glu Tyr Thr Tyr Lys Lys Lys Ile Met Asn Glu Val Asn Asn
 260 265 270
 Asn Asp

(2) INFORMATION FOR SEQ ID NO:5244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5244:

Ser Asp Asp Trp Pro Lys Ser Ile Thr Ser Leu Ser Ile Arg Gly Val
 1 5 10 15
 Arg Met Lys His Gln Glu Thr Thr Ser Gln Gln Tyr Asn Phe Ser Ile
 20 25 30
 Ile Lys His Gly Asp Ile Ser Thr Pro Gln Gly Phe Thr Ala Gly Gly
 35 40 45
 Met His Ile Gly Leu Arg Ala Asn Lys Lys Asp Phe Gly Trp Ile Tyr
 50 55 60
 Ser Ser Ser Leu Ala Ser Ala Ala Ala Val Tyr Thr Leu Asn Gln Phe
 65 70 75 80
 Lys Ala Ala Pro Leu Ile Val Thr Glu Asp Thr Leu Gln Lys Ser Lys
 85 90 95
 Gly Lys Leu Gln Ala Leu Val Val Asn Ser Ala Asn Ala Asn Ser Cys
 100 105 110
 Thr Gly Gln Gln Gly Ile Asp Asp Ala Arg Gln Thr Gln Thr Trp Val
 115 120 125
 Ala Gln Gln Leu Gln Ile Pro Ser Glu His Val Ala Val Ala Ser Thr
 130 135 140
 Gly Val Ile Gly Glu Tyr Leu Pro Met Asp Lys Ile Lys Thr Gly Thr
 145 150 155 160
 Glu His Ile Lys Asp Ala Asn Phe Ala Thr Pro Gly Ala Phe Asn Glu
 165 170 175

Ala Ile Leu Thr Thr Asp Thr Cys Thr Lys His Ile Ala Val Ser Leu
180 185 190

5 Lys Ile Asp Gly Lys Thr Val Thr Ile Gly Gly Ser Thr Lys Gly Ser
195 200 205

Gly Met Ile His Pro Asn Met Ala Thr Met Leu Ala Phe Ile Thr Thr
210 215 220

10 Asp Ala Ser Ile Glu Ser Asn Thr Leu His Gln Leu Leu Lys Ser Ser
225 230 235 240

Thr Asp His Thr Phe Asn Met Ile Thr Val Asp Gly Asp Thr Ser Thr
245 250 255

15 Asn Asp Met Val Leu Val Met Ala Asn His Gln Val Glu His Gln Ile
260 265 270

20 Leu Ser Gln Asp His Pro Gln Trp Glu Thr Phe Val Asp Ala Phe Asn
275 280 285

Phe Val Cys Thr Phe Leu Ala Lys Ala Ile Ala Arg Asp Gly Glu Gly
290 295 300

25 Ala Thr Lys Leu Ile Ser Val Asn Val Ser Gly Ala Lys Ser Ile Ser
305 310 315 320

Asp Ala Arg Lys Ile Gly Lys Thr Ile Val Ser Ser Asn Leu Val Lys
325 330 335

30 Ser Ala Ile Phe Gly Glu Asp Ala Asn Phe Gly Arg Ile Ile Thr Ala
340 345 350

Ile Gly Tyr Ser Gly Cys Glu Ile Asp Pro Asn Cys Thr Tyr Val Gln
355 360 365

35 Leu Asn Gln Ile Pro Val Val Asp Lys Gly Met Ala Val Leu Phe Asp
370 375 380

Glu Gln Ala Met Ser Asn Thr Leu Thr His Glu Asn Val Thr Ile Asp
385 390 395 400

40 Val Gln Leu Gly Leu Gly Asn Ala Ala Ala Thr Ala Tyr Gly Cys Asp
405 410 415

45 Leu Ser Tyr Asp Tyr Val Arg Ile Asn Ala Ser Tyr Arg Thr
420 425 430

(2) INFORMATION FOR SEQ ID NO:5245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5245:

5 Asn Pro Ala Leu Thr Val Phe Ala Phe Ile Met Ile Ile Ser Ile Leu
 1 5 10 15
 Leu Ala Tyr Val Phe Lys Trp Leu Gly Leu Val Asp Asp Val Leu Leu
 20 25 30
 10 Met Val Ile Ile Ile Ser Thr Ile Ser Leu Gly Val Val Val Pro Thr
 35 40 45
 Leu Lys Glu Met Asn Ile Met Arg Thr Thr Ile Gly Gln Phe Ile Leu
 50 55 60
 15 Leu Val Ala Val Leu Ala Asp Leu Val Thr Met Ile Leu Leu Thr Val
 65 70 75 80
 Tyr Gly Ala Ile Asn Gly Gln Gly Gly Ser Thr Ile Trp Leu Ile Gly
 85 90 95
 20 Ile Leu Val Val Phe Thr Ala Ile Ser Tyr Ile Leu Gly Val Gln Phe
 100 105 110
 Lys Arg Met Ser Phe Leu Gln Lys Leu Met Asp Gly Thr Thr Gln Ile
 115 120 125
 25 Gly Ile Arg Ala Val Phe Ala Leu Ile Ile Leu Leu Val Ala Leu Ala
 130 135 140
 Glu Gly Val Gly Ala Glu Asn Ile Leu Gly Ala Phe Leu Ala Gly Val
 145 150 155 160
 Val Val Ser Leu Leu Asn Pro Asp Glu Glu Met Val Glu Lys Leu Asp
 165 170 175
 35 Ser Phe Gly Tyr Gly Phe Phe Ile Pro Ile Phe Phe Ile Met Xaa Gly
 180 185 190
 Val Asp Leu Asn Ile Pro Ser Leu Ile Lys Glu Pro Lys Leu Leu Ile
 195 200 205
 40 Ile Ile Pro Ile Leu Ile Val Ala Phe Ile Ile Ser Lys Leu Ile Pro
 210 215 220
 Val Met Phe Ile Arg Arg Trp Phe Asp Met Lys Thr Thr Ile Ala Ser
 225 230 235 240
 45 Ala Phe Leu Leu Thr Ser Thr Leu Ser Leu Val Ile Ala Ala Ala Lys
 245 250 255
 Ile Ser Glu Arg Leu Asn Ala Ile Ser Ala Glu Thr Ser Gly Ile Leu
 260 265 270
 50 Ile Leu Ser Ala Val Ile Thr Cys Val Phe Val Pro Ile Ile Phe Lys
 275 280 285
 55 Lys Leu Phe Pro Val Pro Asp Glu Phe Asn Arg Lys Ile Glu Val Ser
 290 295 300

EP 0 786 519 A2

Leu Ile Gly Lys Asn Gln Leu Thr Ile Pro Ile Ala Gln Asn Leu Thr
 305 310 315 320
 Ser Gln Leu Tyr Asp Val Thr Leu Tyr Tyr Arg Lys Asp Leu Ser Asp
 5 325 330 335
 Arg Arg Gln Leu Ser Asp Asp Ile Thr Met Ile Glu Ile Ala Asp Tyr
 340 345 350
 Glu Gln Asp Val Leu Glu Arg Leu Gly Leu Phe Asp Arg Asp Ile Val
 10 355 360 365
 Val Cys Ala Thr Asn Asp Asp Asp Ile Asn Arg Lys Val Ala Lys Leu
 370 375 380
 Ala Lys Ala His Gln Val Glu Arg Val Ile Cys Arg Leu Glu Ser Thr
 15 385 390 395 400
 Thr Asp Asp Thr Glu Leu Val Asp Ser Gly Ile Glu Ile Phe Ser Ser
 20 405 410 415
 Tyr Leu Ser Asn Lys Ile Leu Leu Lys Gly Leu Ile Glu Thr Pro Asn
 420 425 430
 Met Leu Asn Leu Leu Ser Asn Val Glu Thr Ser Leu Tyr Glu Ile Gln
 25 435 440 445
 Met Leu Asn Tyr Lys Tyr Glu Asn Ile Gln Leu Arg Asn Phe Pro Phe
 450 455 460
 Gly Gly Asp Ile Ile
 30 465

(2) INFORMATION FOR SEQ ID NO:5246:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 414 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5246:

Ala Ile Ile Val Ile Leu Leu Phe Leu Arg Asn Ile Arg Thr Thr Ala
 1 5 10 15
 Ile Ser Ile Ile Ser Ile Pro Leu Ser Leu Leu Met Ala Leu Ile Ala
 50 20 25 30
 Leu Lys Leu Ser Asp Val Ser Leu Asn Ile Leu Thr Leu Gly Ala Leu
 35 40 45
 Thr Val Ala Ile Gly Arg Val Ile Asp Asp Ser Ile Val Val Val Glu
 55 50 55 60

EP 0 786 519 A2

	Asn	Ile	Tyr	Arg	Arg	Leu	Thr	Asp	Ser	Glu	Glu	Gln	Leu	Lys	Gly	Glu	65	70	75	80
5	Asn	Leu	Ile	Ile	Ser	Ala	Thr	Thr	Glu	Val	Phe	Lys	Pro	Ile	Met	Ser		85	90	95
	Ser	Thr	Leu	Val	Thr	Ile	Ile	Val	Phe	Leu	Pro	Leu	Val	Phe	Val	Ser		100	105	110
10	Gly	Ser	Val	Gly	Glu	Met	Phe	Arg	Pro	Phe	Ala	Leu	Ala	Ile	Ala	Phe		115	120	125
	Ser	Leu	Leu	Ala	Ser	Leu	Leu	Val	Ser	Ile	Thr	Leu	Val	Pro	Ala	Leu		130	135	140
15	Ala	Ala	Thr	Leu	Phe	Lys	Lys	Gly	Val	Lys	Arg	Arg	Asn	Lys	Gln	His		145	150	155
	Gln	Glu	Gly	Leu	Gly	Val	Val	Ser	Thr	Thr	Tyr	Lys	Lys	Val	Leu	His		165	170	175
20	Trp	Ser	Leu	Asn	His	Lys	Trp	Ile	Val	Ile	Ile	Leu	Ser	Thr	Leu	Ile		180	185	190
	Leu	Val	Ala	Thr	Ile	Val	Phe	Gly	Gly	Pro	Arg	Leu	Gly	Thr	Ser	Phe		195	200	205
25	Ile	Ser	Ala	Gly	Asp	Asp	Lys	Phe	Leu	Ala	Ile	Thr	Tyr	Thr	Pro	Lys		210	215	220
	Pro	Gly	Glu	Thr	Glu	Gln	Ala	Val	Leu	Asn	His	Ala	Lys	Asp	Val	Glu		225	230	235
30	Lys	Tyr	Leu	Lys	Gln	Lys	Lys	His	Val	Lys	Thr	Ile	Gln	Tyr	Ser	Val		245	250	255
	Gly	Gly	Ser	Ser	Pro	Val	Asp	Pro	Thr	Gly	Ser	Thr	Asn	Ser	Met	Ala		260	265	270
35	Ile	Met	Val	Glu	Tyr	Asp	Asn	Asp	Thr	Pro	Asn	Phe	Asp	Val	Glu	Ala		275	280	285
40	Asp	Lys	Val	Ile	Lys	His	Ala	Asp	Gly	Phe	Lys	His	Pro	Gly	Glu	Trp		290	295	300
	Lys	Asn	Gln	Asp	Leu	Gly	Thr	Gly	Ala	Gly	Asn	Lys	Ser	Val	Glu	Val		305	310	315
45	Thr	Val	Lys	Gly	Pro	Ser	Met	Asp	Ala	Ile	Lys	Ser	Thr	Val	Lys	Asp		325	330	335
	Ile	Glu	Gln	Lys	Met	Lys	Gln	Val	Lys	Gly	Leu	Ala	Asn	Val	Lys	Ser		340	345	350
50	Asp	Leu	Ser	Gln	Thr	Tyr	Asp	Gln	Tyr	Glu	Ile	Lys	Val	Asp	Gln	Asn		355	360	365
55	Lys	Ala	Ala	Glu	Asn	Gly	Ile	Ser	Ala	Ser	Gln	L	u	Ala	Met	His		370	375	380

Asn Glu Asn Leu Pro Glu Lys Thr Val Thr Thr Val Lys Glu Asn Gly
 385 390 395 400
 Lys Thr Val Asp Val Lys Val Lys Gln Asn Lys Gln Thr Ala
 405 410

(2) INFORMATION FOR SEQ ID NO:5247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5247:

Gly Lys Pro Phe Ile Ile Gly Leu Gly Asp Ile Ile Val Lys Lys Leu
 1 5 10 15
 Thr Thr Ile Leu Phe Gln Tyr Lys Ile Phe Pro Val Leu Met Phe Leu
 20 25 30
 Val Ser Thr Gly Leu Gly Ile Ile Val Ile Thr Gln Asn Ile Leu Ile
 35 40 45
 Ala Asp Phe Leu Ala Lys Ile Ile Arg His Gln Phe Gln Gly Leu Trp
 50 55 60
 Ile Val Leu Phe Ile Leu Leu Gly Val Leu Leu Arg Ala Thr Val
 65 70 75 80
 Gln Phe Leu Asn Gln Trp Leu Gly Asp Thr Leu Ala Phe Lys Val Lys
 85 90 95
 His Met Leu Arg Gln Arg Val Ile Tyr Lys Asn Asn Gly His Pro Ile
 100 105 110
 Gly Glu Gln Met Thr Ile Leu Thr Glu Asn Ile Asp Gly Leu Ala Pro
 115 120 125
 Phe Tyr Lys Ser Tyr Leu Pro Gln Val Phe Lys Ser Met Met Val Pro
 130 135 140
 Leu Ile Ile Ile Ile Ala Met Phe Phe Ile His Phe Asn Thr Ala Leu
 145 150 155 160
 Ile Met Leu Ile Thr Ala Pro Phe Ile Pro Leu Phe Tyr Ile Ile Phe
 165 170 175
 Gly Leu Lys Thr Arg Asp Glu Ser Lys Asp Gln Met Thr Tyr Leu Asn
 180 185 190
 Gln Phe Ser Gln Arg Phe Leu Asn Ile Ala Lys Gly Leu Val Thr Leu
 195 200 205

	Lys	Leu	Phe	Asn	Arg	Thr	Glu	Gln	Thr	Glu	Lys	His	Ile	Tyr	Asp	Asp	
	210						215					220					
5	Ser	Thr	Gln	Phe	Arg	Thr	Leu	Thr	Met	Arg	Ile	Leu	Arg	Ser	Ala	Phe	
	225					230					235					240	
	Leu	Ser	Gly	Leu	Met	Leu	Glu	Phe	Ile	Ser	Met	Leu	Gly	Ile	Gly	Leu	
					245					250					255		
10	Val	Ala	Leu	Glu	Ala	Thr	Leu	Ser	Leu	Val	Val	Phe	His	Asn	Ile	Asp	
				260					265					270			
	Phe	Lys	Thr	Ala	Ala	Ile	Ala	Ile	Ile	Leu	Ala	Pro	Glu	Phe	Tyr	Asn	
			275					280					285				
15	Ala	Ile	Lys	Asp	Leu	Gly	Gln	Ala	Phe	His	Thr	Gly	Lys	Gln	Ser	Glu	
	290					295						300					
	Gly	Ala	Ser	Asp	Val	Val	Phe	Glu	Phe	Leu	Glu	Gln	Pro	Asn	Tyr	Asn	
	305				310						315					320	
20	Asn	Glu	Phe	Leu	Leu	Lys	Tyr	Glu	Glu	Asn	Gln	Lys	Pro	Phe	Ile	Gln	
				325						330					335		
	Leu	Thr	Asp	Ile	Ser	Phe	Arg	Tyr	Asp	Asp	Ser	Asp	Arg	Leu	Val	Leu	
25			340						345					350			
	Asn	Asp	Leu	Asn	Leu	Glu	Ile	Phe	Lys	Gly	Asp	Gln	Ile	Ala	Leu	Val	
			355					360					365				
30	Gly	Pro	Ser	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Thr	His	Leu	Ile	Ala	Gly	
	370					375						380					
	Val	Tyr	Gln	Pro	Thr	Ile	Gly	Thr	Ile	Ser	Thr	Asn	Gln	Arg	Asp	Leu	
	385				390						395					400	
35	Asn	Ile	Gly	Ile	Leu	Ser	Gln	Gln	Pro	Tyr	Ile	Phe	Ser	Ala	Ser	Ile	
					405					410					415		
	Lys	Glu	Asn	Ile	Thr	Met	Phe	Lys	Asp	Ile	Glu	Asn	Asn	Thr	Ile	Glu	
				420					425					430			
40	Glu	Val	Leu	Asp	Glu	Val	Gly	Leu	Leu	Asp	Lys	Val	Gln	Ser	Phe	Thr	
			435				440						445				
	Lys	Gly	Ile	Asn	Thr	Ile	Ile	Gly	Glu	Gly	Gly	Glu	Met	Leu	Ser	Gly	
		450					455					460					
45	Gly	Gln	Met	Arg	Arg	Ile	Glu	Leu	Cys	Arg	Leu	Leu	Val	Met	Lys	Pro	
	465				470					475					480		
	Asp	Leu	Val	Ile	Phe	Asp	Glu	Pro	Ala	Thr	Gly	Leu	Asp	Ile	Gln	Thr	
				485						490					495		
50	Glu	His	Met	Ile	Gln	Asn	Val	Leu	Phe	Gln	His	Phe	Lys	Asp	Thr	Thr	
				500					505					510			
55	Met	Ile	Val	Ile	Ala	His	Arg	Asp	Asn	Thr	Ile	Arg	His	Leu	Gln	Arg	
			515					520					525				

Arg Leu Tyr Ile Glu Asn Gly Arg Leu Ile Ala Asp Asp Arg Asn Ile
 530 535 540

Ser Val Asn Ile Thr Glu Asn Gly Asp Asp Leu
 545 550 555

(2) INFORMATION FOR SEQ ID NO:5248:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5248:

Val Trp Lys Leu Lys Met Arg Trp Ile Lys Arg Lys Lys Lys Asn Phe
 1 5 10 15

Leu Asn Ser Lys Phe Asn Phe Asn Asn Gly Lys Ile Ala Thr Tyr Leu
 20 25 30

Tyr Lys Glu Arg Thr Ala Met Trp Asn Lys Asn Arg Leu Thr Gln Met
 35 40 45

Leu Ser Ile Glu Tyr Pro Ile Ile Gln Ala Gly Met Ala Gly Ser Thr
 50 55 60

Thr Pro Lys Leu Val Ala Ser Val Ser Asn Ser Gly Gly Leu Gly Thr
 65 70 75 80

Ile Gly Ala Gly Tyr Phe Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp
 85 90 95

Tyr Val Arg Gln Leu Thr Ser Asn Ser Phe Gly Val Asn Val Phe Val
 100 105 110

Pro Ser Gln Gln Ser Tyr Thr Ser Ser Gln Ile Glu Asn Met Asn Ala
 115 120 125

Trp Leu Lys Pro Tyr Arg Arg Ala Leu His Leu Glu Glu Pro Val Val
 130 135 140

Lys Ile Thr Glu Glu Gln Gln Phe Lys Cys His Ile Asp Thr Ile Ile
 145 150 155 160

Lys Lys Gln Val Pro Val Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu
 165 170 175

Gln Ile Ile Ser Arg Leu Lys Ala Ala Asn Val Lys Leu Ile Gly Thr
 180 185 190

Ala Thr Ser Val Asp Glu Ala Ile Ala Asn Glu Lys Ala Gly Met Asp
 195 200 205

EP 0 786 519 A2

Ala Ile Val Ala Gln Gly Ser Glu Ala Gly Gly His Arg Gly Ser Phe
 210 215 220

5 Leu Lys Pro Lys Asn Gln Leu Pro Met Val Gly Thr Ile Ser Leu Val
 225 230 235 240

Pro Gln Ile Val Asp Val Val Ser Ile Pro Val Ile Ala Ala Gly Gly
 245 250 255

10 Ile Met Asp Gly Arg Gly Val Leu Ala Ser Ile Val Leu Gly Ala Glu
 260 265 270

Gly Val Gln Met Gly Thr Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala
 275 280 285

15 Ser Glu Leu Leu Arg Asp Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr
 290 295 300

Val Ile Thr Lys Ala Phe Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn
 305 310 315 320

20 Arg Phe Ile Glu Glu Met Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr
 325 330 335

Pro Ile Gln Asn Glu Leu Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn
 340 345 350

25 Ile Gly Asp Lys Glu Leu Ile His Met Trp Ser Gly Gln Ser Pro Arg
 355 360 365

Leu Ala Thr Thr His Pro Ala Asn Thr Ile Met Ser Asn Ile Ile Asn
 370 375 380

Gln Ile Asn Gln Ile Met Gln Tyr Lys
 385 390

(2) INFORMATION FOR SEQ ID NO:5249:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 936 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5249:

Asn Asp Phe Leu Lys Arg Gly Asn Lys Met Asn Met Lys Lys Lys Glu
 1 5 10 15

Lys His Ala Ile Arg Lys Lys Ser Ile Gly Val Ala Ser Val Leu Val
 20 25 30

Gly Thr Leu Ile Gly Phe Gly Leu Ser Ser Lys Glu Ala Asp Ala
 35 40 45

EP 0 786 519 A2

	Ser	Glu	Asn	Ser	Val	Thr	Gln	Ser	Asp	Ser	Ala	Ser	Asn	Glu	Ser	Lys
	50						55					60				
5	Ser	Asn	Asp	Ser	Ser	Ser	Val	Ser	Ala	Ala	Pro	Lys	Thr	Asp	Asp	Thr
	65					70					75					80
	Asn	Val	Ser	Asp	Thr	Lys	Thr	Ser	Ser	Asn	Thr	Asn	Asn	Gly	Glu	Thr
					85					90					95	
10	Ser	Val	Ala	Gln	Asn	Pro	Ala	Gln	Gln	Glu	Thr	Thr	Gln	Ser	Ser	Ser
				100					105					110		
	Thr	Asn	Ala	Thr	Thr	Glu	Glu	Thr	Pro	Val	Thr	Gly	Glu	Ala	Thr	Thr
			115					120					125			
15	Thr	Thr	Thr	Asn	Gln	Ala	Asn	Thr	Pro	Ala	Thr	Thr	Gln	Ser	Ser	Asn
	130						135					140				
	Thr	Asn	Ala	Glu	Glu	Leu	Val	Asn	Gln	Thr	Ser	Asn	Glu	Thr	Thr	Ser
	145					150					155					160
20	Asn	Asp	Thr	Asn	Thr	Val	Ser	Ser	Val	Asn	Ser	Pro	Gln	Asn	Ser	Thr
					165					170					175	
	Asn	Ala	Glu	Asn	Val	Ser	Thr	Thr	Gln	Asp	Thr	Ser	Thr	Glu	Ala	Thr
25				180					185					190		
	Pro	Ser	Asn	Asn	Glu	Ser	Ala	Pro	Gln	Ser	Thr	Asp	Ala	Ser	Asn	Lys
			195					200					205			
30	Asp	Val	Val	Asn	Gln	Ala	Val	Asn	Thr	Ser	Ala	Pro	Arg	Met	Arg	Ala
	210						215					220				
	Phe	Ser	Leu	Ala	Ala	Val	Ala	Ala	Asp	Ala	Pro	Val	Ala	Gly	Thr	Asp
	225					230					235					240
35	Ile	Thr	Asn	Gln	Leu	Thr	Asn	Val	Thr	Val	Gly	Ile	Asp	Ser	Gly	Thr
					245					250					255	
	Thr	Val	Tyr	Pro	His	Gln	Ala	Gly	Tyr	Val	Lys	Leu	Asn	Tyr	Gly	Phe
				260					265					270		
40	Ser	Val	Pro	Asn	Ser	Ala	Val	Lys	Gly	Asp	Thr	Phe	Lys	Ile	Thr	Val
			275					280					285			
	Pro	Lys	Glu	Leu	Asn	Leu	Asn	Gly	Val	Thr	Ser	Thr	Ala	Lys	Val	Pro
		290					295					300				
45	Pro	Ile	Met	Ala	Gly	Asp	Gln	Val	Leu	Ala	Asn	Gly	Val	Ile	Asp	Ser
	305					310					315				320	
	Asp	Gly	Asn	Val	Ile	Tyr	Thr	Phe	Thr	Asp	Tyr	Val	Asn	Thr	Lys	Asp
50					325					330					335	
	Asp	Val	Lys	Ala	Thr	Leu	Thr	Met	Pro	Ala	Tyr	Ile	Asp	Pro	Glu	Asn
				340					345					350		
55	Val	Lys	Lys	Thr	Gly	Asn	Val	Thr	Leu	Ala	Thr	Gly	Ile	Gly	Ser	Thr
			355					360					365			

EP 0 786 519 A2

	Thr	Ala	Asn	Lys	Thr	Val	Leu	Val	Asp	Tyr	Glu	Lys	Tyr	Gly	Lys	Phe
	370						375					380				
5	Tyr	Asn	Leu	Ser	Ile	Lys	Gly	Thr	Ile	Asp	Gln	Ile	Asp	Lys	Thr	Asn
	385					390					395					400
	Asn	Thr	Tyr	Arg	Gln	Thr	Ile	Tyr	Val	Asn	Pro	Ser	Gly	Asp	Asn	Val
					405					410					415	
10	Ile	Ala	Pro	Val	Leu	Thr	Gly	Asn	Leu	Lys	Pro	Asn	Thr	Asp	Ser	Asn
				420					425					430		
	Ala	Leu	Ile	Asp	Gln	Gln	Asn	Thr	Ser	Ile	Lys	Val	Tyr	Lys	Val	Asp
			435					440						445		
15	Asn	Ala	Ala	Asp	Leu	Ser	Glu	Ser	Tyr	Phe	Val	Asn	Pro	Glu	Asn	Phe
	450						455					460				
	Glu	Asp	Val	Thr	Asn	Ser	Val	Asn	Ile	Thr	Phe	Pro	Asn	Pro	Asn	Gln
	465					470					475					480
20	Tyr	Lys	Val	Glu	Phe	Asn	Thr	Pro	Asp	Asp	Gln	Ile	Thr	Thr	Pro	Tyr
					485					490					495	
	Ile	Val	Val	Val	Asn	Gly	His	Ile	Asp	Pro	Asn	Ser	Lys	Gly	Asp	Leu
25					500				505					510		
	Ala	Leu	Arg	Ser	Thr	Leu	Tyr	Gly	Tyr	Asn	Ser	Asn	Ile	Ile	Trp	Arg
			515					520						525		
30	Ser	Met	Ser	Trp	Asp	Asn	Glu	Val	Ala	Phe	Asn	Asn	Gly	Ser	Gly	Ser
	530						535					540				
	Gly	Asp	Gly	Ile	Asp	Lys	Pro	Val	Val	Pro	Glu	Gln	Pro	Asp	Glu	Pro
	545					550					555					560
35	Gly	Glu	Ile	Glu	Pro	Ile	Pro	Glu	Asp	Ser	Asp	Ser	Asp	Pro	Gly	Ser
					565					570					575	
	Asp	Ser	Gly	Ser	Asp	Ser	Asn	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Gly	Ser
				580					585					590		
40	Asp	Ser	Thr	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser
			595					600					605			
	Ala	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser
			610				615					620				
45	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Ser	Asp	Ser
	625					630					635				640	
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					645				650						655	
50	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					660				665					670		
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
55					675				680					685		

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 690 695 700
 5 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 705 710 715 720
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 725 730 735
 10 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 740 745 750
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 755 760 765
 15 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Asp Ser
 770 775 780
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 785 790 795 800
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 805 810 815
 25 Glu Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 820 825 830
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Gly Ser
 835 840 845
 30 Asp Ser Asp Ser Ser Ser Asp Ser Asp Ser Asp Ser Glu Ser Asp Ser Asn Ser
 850 855 860
 Asp Ser Glu Ser Val Ser Asn Asn Asn Val Val Pro Pro Asn Ser Pro
 865 870 875 880
 35 Lys Asn Gly Thr Asn Ala Ser Asn Lys Asn Glu Ala Lys Asp Ser Lys
 885 890 895
 Glu Pro Leu Pro Asp Thr Gly Ser Glu Asp Glu Ala Asn Thr Ser Leu
 900 905 910
 Ile Trp Gly Leu Leu Ala Ser Ile Gly Ser Leu Leu Leu Phe Arg Arg
 915 920 925
 45 Lys Lys Glu Asn Lys Asp Lys Lys
 930 935

(2) INFORMATION FOR SEQ ID NO:5250:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 194 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5250:

Val Ser Lys Leu Lys Lys Glu Ile Leu Glu Trp Ile Ile Ser Ile Ala
 1 5 10 15
 Val Ala Phe Val Ile Leu Phe Ile Val Gly Lys Phe Ile Val Thr Pro
 20 25 30
 Tyr Thr Ile Lys Gly Glu Ser Met Asp Pro Thr Leu Lys Asp Gly Glu
 35 40 45
 Arg Val Ala Val Asn Ile Val Gly Tyr Lys Thr Gly Gly Leu Glu Lys
 50 55 60
 Gly Asn Val Val Val Phe His Ala Asn Lys Asn Asp Asp Tyr Val Lys
 65 70 75 80
 Arg Val Ile Gly Val Pro Gly Asp Lys Val Glu Tyr Lys Asn Asp Thr
 85 90 95
 Leu Tyr Val Asn Gly Lys Lys Gln Asp Glu Pro Tyr Leu Asn Tyr Asn
 100 105 110
 Leu Lys His Lys Gln Gly Asp Tyr Ile Thr Gly Thr Phe Gln Val Lys
 115 120 125
 Asp Leu Pro Asn Ala Asn Pro Lys Ser Asn Val Ile Pro Lys Gly Lys
 130 135 140
 Tyr Leu Val Leu Gly Asp Asn Arg Glu Val Ser Lys Asp Ser Arg Ala
 145 150 155 160
 Phe Gly Leu Ile Asp Glu Asp Gln Ile Val Gly Lys Val Ser Phe Gln
 165 170 175
 Val Leu Ala His Phe Ser Glu Phe Gln Thr Ser Ile Ser Xaa Leu Lys
 180 185 190
 Ile Leu

(2) INFORMATION FOR SEQ ID NO:5251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5251:

Leu Lys Ala Xaa Tyr Ala Lys Leu Asp Asp Val Ser Lys Phe Glu Asp
 1 5 10 15

	Val	Thr	Asp	Asn	Met	Ser	Leu	Asp	Phe	Asp	Thr	Asn	Gly	Gly	Tyr	Ser	
				20					25					30			
5	Leu	Asn	Phe	Asn	Asn	Leu	Asp	Gln	Ser	Lys	Asn	Tyr	Val	Ile	Lys	Tyr	
			35				40						45				
	Glu	Gly	Tyr	Tyr	Asp	Ser	Asn	Ala	Ser	Asn	Leu	Glu	Phe	Gln	Thr	His	
		50					55					60					
10	Leu	Phe	Gly	Tyr	Tyr	Asn	Tyr	Tyr	Tyr	Thr	Ser	Asn	Leu	Thr	Trp	Lys	
	65					70					75					80	
	Asn	Gly	Val	Ala	Phe	Tyr	Ser	Asn	Asn	Ala	Gln	Gly	Asp	Gly	Lys	Asp	
					85					90					95		
15	Lys	Leu	Lys	Glu	Pro	Ile	Ile	Glu	His	Ser	Thr	Pro	Ile	Glu	Leu	Glu	
				100					105					110			
	Phe	Lys	Ser	Glu	Pro	Pro	Val	Glu	Lys	His	Glu	Leu	Thr	Gly	Thr	Ile	
20			115					120					125				
	Glu	Glu	Ser	Asn	Asp	Ser	Lys	Pro	Ile	Asp	Phe	Glu	Tyr	His	Thr	Ala	
		130					135					140					
25	Val	Glu	Gly	Ala	Glu	Gly	His	Ala	Glu	Gly	Thr	Ile	Glu	Thr	Glu	Glu	
	145					150					155					160	
	Asp	Ser	Ile	His	Val	Asp	Phe	Glu	Glu	Ser	Thr	His	Glu	Asn	Ser	Lys	
					165					170					175		
30	His	His	Ala	Asp	Val	Val	Glu	Tyr	Glu	Glu	Asp	Thr	Asn	Pro	Gly	Gly	
				180					185					190			
	Gly	Gln	Val	Thr	Thr	Glu	Ser	Asn	Leu	Val	Glu	Phe	Asp	Glu	Asp	Ser	
			195					200					205				
35	Thr	Lys	Gly	Ile	Val	Thr	Gly	Ala	Val	Ser	Asp	His	Thr	Thr	Ile	Glu	
		210					215					220					
	Asp	Thr	Lys	Glu	Tyr	Thr	Thr	Glu	Ser	Asn	Leu	Ile	Glu	Leu	Val	Asp	
	225					230					235					240	
40	Glu	Leu	Pro	Glu	Glu	His	Gly	Gln	Ala	Gln	Gly	Pro	Ile	Glu	Glu	Ile	
					245					250					255		
	Thr	Glu	Asn	Asn	His	His	Ile	Ser	His	Ser	Gly	Leu	Gly	Thr	Glu	Asn	
45				260					265					270			
	Gly	His	Gly	Asn	Tyr	Gly	Val	Ile	Glu	Glu	Ile	Glu	Glu	Asn	Ser	His	
			275					280					285				
50	Val	Asp	Ile	Lys	Ser	Glu	Leu	Gly	Tyr	Glu	Gly	Gly	Gln	Asn	Ser	Gly	
		290					295					300					
	Asn	Gln	Ser	Phe	Glu	Glu	Asp	Thr	Glu	Glu	Asp	Lys	Pro	Lys	Tyr	Glu	
	305					310					315					320	
55	Gln	Gly	Gly	Asn	Ile	Val	Asp	Ile	Asp	Phe	Asp	Ser	Val	Pro	Gln	Ile	
				325						330					335		

His Gly Gln Asn Asn Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Lys
 340 345 350
 5 Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Ile Asp Ile Asp Phe
 355 360 365
 Asp Ser Val Pro His Ile His Gly Phe Asn Lys His Thr Glu Ile Ile
 370 375 380
 10 Glu Glu Asp Thr Asn Lys Asp Lys Pro Asn Tyr Gln Phe Gly Gly His
 385 390 395 400
 Asn Ser Val Asp Phe Glu Glu Asp Thr Leu Pro Gln Val Ser Gly His
 405 410 415
 15 Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp Thr Thr Pro Pro Ile Val
 420 425 430
 Pro Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro
 435 440 445
 20 Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro Thr Pro
 450 455 460
 Pro Thr Pro Glu Val Pro Thr Glu Pro Gly Lys Pro Ile Pro Pro Ala
 465 470 475 480
 25 Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu Gln Gly Lys Val
 485 490 495
 Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys Ala Val Val Pro
 500 505 510
 30 Thr Lys Lys Ala Gln Ser Lys Lys Ser Glu Leu Pro Glu Thr Gly Gly
 515 520 525
 35 Glu Glu Ser Thr Asn Asn Gly Met Leu Phe Gly Gly Leu Phe Ser Ile
 530 535 540
 Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys Lys Asn His Lys Ala
 545 550 555

(2) INFORMATION FOR SEQ ID NO:5252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5252:

Thr Lys Asn Glu Lys Ile Asn Asp Val Thr Ala Val Ala Glu Lys Glu
 1 5 10 15

Val Val Glu Glu Thr Lys Ala Thr Gly Thr Asp Val Thr Asn Lys Val
 20 25 30
 Glu Val Glu Glu Gly Ser Glu Ile Val Gly His Lys Gln Asp Thr Asn
 35 40 45
 Val Val Asn Pro His Asn Ala Glu Arg Val Thr Leu Lys Tyr Lys Trp
 50 55 60
 Lys Phe Gly Glu Gly Ile Lys Ala Gly Asp Tyr Phe Asp Phe Thr Leu
 65 70 75 80
 Ser Asp Asn Val Glu Thr His Gly Ile Ser Thr Leu Arg Lys Val Pro
 85 90 95
 Glu Ile Lys Ser Thr Asp Gly Gln Val Met Ala Thr Gly Glu Ile Ile
 100 105 110
 Gly Glu Arg Lys Val Arg Tyr Thr Phe Lys Glu Tyr Val Gln Glu Lys
 115 120 125
 Lys Asp Leu Thr Ala Glu Leu Ser Leu Asn Leu Phe Ile Asp Pro Thr
 130 135 140
 Thr Val Thr Gln Lys Gly Asn Gln Asn Val Glu Val Lys Leu Gly Glu
 145 150 155 160
 Thr Thr Val Ser Lys Ile Phe Asn Ile Gln Tyr Leu Gly Gly Val Arg
 165 170 175
 Asp Asn Trp Gly Val Thr Ala Asn Gly Arg Ile Asp Thr Leu Asn Lys
 180 185 190
 Val Asp Gly Lys Phe Ser His Phe Ala Tyr Met Lys Pro Asn Asn Gln
 195 200 205
 Ser Leu Ser Ser Val Thr Val Thr Gly Gln Val Thr Lys Gly Asn Lys
 210 215 220
 Pro Gly Val Asn Asn Pro Thr Val Lys Val Tyr Lys His Ile Gly Ser
 225 230 235 240
 Asp Asp Leu Ala Glu Ser Xaa Xaa Cys Lys Ala
 245 250

(2) INFORMATION FOR SEQ ID NO:5253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5253:

1 Ile Leu His Leu Arg Glu Asn Ile Ile Val Lys Ser Asn Leu Arg Tyr
 5 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr
 10 Met Ile Val Val Gly Met Gly Gln Glu Lys Glu Ala Ala Ala Ser Glu
 15 Gln Asn Asn Thr Thr Val Glu Glu Ser Gly Ser Ser Ala Thr Glu Ser
 20 Lys Ala Ser Glu Thr Gln Thr Thr Thr Asn Asn Val Asn Thr Ile Asp
 25 Glu Thr Gln Ser Tyr Ser Ala Thr Ser Thr Glu Gln Pro Ser Gln Ser
 30 Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Thr Val Gln Ala Pro Lys
 35 Val Glu Thr Ser Arg Val Asp Leu Pro Ser Glu Lys Val Ala Asp Lys
 40 Glu Thr Thr Gly Thr Gln Val Asp Ile Ala Gln Pro Ser Asn Val Ser
 45 Glu Ile Lys Pro Arg Met Lys Arg Ser Met Thr Leu Gln Gln Leu Gln
 50 Arg Lys Lys

(2) INFORMATION FOR SEQ ID NO:5254:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1027 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5254:

1 Ile Leu His Leu Lys Gly Asp Ile Ile Val Lys Asn Asn Leu Arg Tyr
 5 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr
 10 Met Ile Val Val Gly Met Gly Gln Asp Lys Glu Ala Ala Ala Ser Glu
 15 Gln Lys Thr Thr Thr Val Glu Glu Asn Gly Asn Ser Ala Thr Asp Asn
 20 25 30 35 40 45 50 55 60

EP 0 786 519 A2

Lys Thr Ser Glu Thr Gln Thr Thr Ala Thr Asn Val Asn His Ile Glu
 65 70 75 80
 5 Glu Thr Gln Ser Tyr Asn Ala Thr Val Thr Glu Gln Pro Ser Asn Ala
 85 90 95
 Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Ala Val Gln Ala Pro Gln
 100 105 110
 10 Thr Ala Gln Pro Ala Asn Ile Glu Thr Val Lys Glu Glu Val Val Lys
 115 120 125
 Glu Glu Ala Lys Pro Gln Val Lys Glu Thr Thr Gln Ser Gln Asp Asn
 130 135 140
 15 Ser Gly Asp Gln Arg Gln Val Asp Leu Thr Pro Lys Lys Ala Thr Gln
 145 150 155 160
 Asn Gln Val Ala Glu Thr Gln Val Glu Val Ala Gln Pro Arg Thr Ala
 165 170 175
 20 Ser Glu Ser Lys Pro Arg Val Thr Arg Ser Ala Asp Val Ala Glu Ala
 180 185 190
 Lys Glu Ala Ser Asn Ala Lys Val Glu Thr Gly Thr Asp Val Thr Ser
 195 200 205
 25 Lys Val Thr Val Glu Ile Gly Ser Ile Glu Gly His Asn Asn Thr Asn
 210 215 220
 Lys Val Glu Pro His Ala Gly Gln Arg Ala Val Leu Lys Tyr Lys Leu
 225 230 235 240
 Lys Phe Glu Asn Gly Leu His Gln Gly Asp Tyr Phe Asp Phe Thr Leu
 245 250 255
 35 Ser Asn Asn Val Asn Thr His Gly Val Ser Thr Ala Arg Lys Val Pro
 260 265 270
 Glu Ile Lys Asn Gly Ser Val Val Met Ala Thr Gly Glu Val Leu Glu
 275 280 285
 40 Gly Gly Lys Ile Arg Tyr Thr Phe Thr Asn Asp Ile Glu Asp Lys Val
 290 295 300
 Asp Val Thr Ala Glu Leu Glu Ile Asn Leu Phe Ile Asp Pro Lys Thr
 305 310 315 320
 45 Val Gln Thr Asn Gly Asn Gln Thr Ile Thr Ser Thr Leu Asn Glu Glu
 325 330 335
 Gln Thr Ser Lys Glu Leu Asp Val Lys Tyr Lys Asp Gly Ile Gly Asn
 340 345 350
 50 Tyr Tyr Ala Asn Leu Asn Gly Ser Ile Glu Thr Phe Asn Lys Ala Asn
 355 360 365
 55 Asn Arg Phe Ser His Val Ala Phe Ile Lys Pro Asn Asn Gly Lys Thr
 370 375 380

EP 0 786 519 A2

	Thr	Ser	Val	Thr	Val	Thr	Gly	Thr	Leu	Met	Lys	Gly	Ser	Asn	Gln	Asn	385	390	395	400
5	Gly	Asn	Gln	Pro	Lys	Val	Arg	Ile	Phe	Glu	Tyr	Leu	Gly	Asn	Asn	Glu		405	410	415
	Asp	Ile	Ala	Lys	Ser	Val	Tyr	Ala	Asn	Thr	Thr	Asp	Thr	Ser	Lys	Phe		420	425	430
10	Lys	Glu	Val	Thr	Ser	Asn	Met	Ser	Gly	Asn	Leu	Asn	Leu	Gln	Asn	Asn		435	440	445
	Gly	Ser	Tyr	Ser	Leu	Asn	Ile	Glu	Asn	Leu	Asp	Lys	Thr	Tyr	Val	Val		450	455	460
15	His	Tyr	Asp	Gly	Glu	Tyr	Leu	Asn	Gly	Thr	Asp	Glu	Val	Asp	Phe	Arg	465	470	475	480
	Thr	Gln	Met	Val	Gly	His	Pro	Glu	Gln	Leu	Tyr	Lys	Tyr	Tyr	Tyr	Asp		485	490	495
20	Arg	Gly	Tyr	Thr	Leu	Thr	Trp	Asp	Asn	Gly	Leu	Val	Leu	Tyr	Ser	Asn		500	505	510
	Lys	Ala	Asn	Gly	Asn	Glu	Lys	Asn	Gly	Pro	Ile	Ile	Gln	Asn	Asn	Lys		515	520	525
25	Phe	Glu	Tyr	Lys	Glu	Asp	Thr	Ile	Lys	Glu	Thr	Leu	Thr	Gly	Gln	Tyr		530	535	540
30	Asp	Lys	Asn	Leu	Val	Thr	Thr	Val	Glu	Glu	Glu	Tyr	Asp	Ser	Ser	Thr	545	550	555	560
	Leu	Asp	Ile	Asp	Tyr	His	Thr	Ala	Ile	Asp	Gly	Gly	Gly	Gly	Tyr	Val		565	570	575
35	Asp	Gly	Tyr	Ile	Glu	Thr	Ile	Glu	Glu	Thr	Asp	Ser	Ser	Ala	Ile	Asp		580	585	590
	Ile	Asp	Tyr	His	Thr	Ala	Val	Asp	Ser	Glu	Ala	Gly	His	Val	Gly	Gly		595	600	605
40	Tyr	Thr	Glu	Ser	Ser	Glu	Glu	Ser	Asn	Pro	Ile	Asp	Phe	Glu	Glu	Ser		610	615	620
	Thr	His	Glu	Asn	Ser	Lys	His	His	Ala	Asp	Val	Val	Glu	Tyr	Glu	Glu	625	630	635	640
45	Asp	Thr	Asn	Pro	Gly	Gly	Gly	Gln	Val	Thr	Thr	Glu	Ser	Asn	Leu	Val		645	650	655
	Glu	Phe	Asp	Glu	Glu	Ser	Thr	Lys	Gly	Ile	Val	Thr	Gly	Ala	Val	Ser		660	665	670
50	Asp	His	Thr	Thr	Val	Glu	Asp	Thr	Lys	Glu	Tyr	Thr	Thr	Glu	Ser	Asn		675	680	685
55	Leu	Ile	Glu	Leu	Val	Asp	Glu	Leu	Pro	Glu	Glu	His	Gly	Gln	Ala	Gln		690	695	700

	Gly	Pro	Val	Glu	Glu	Ile	Thr	Lys	Asn	Asn	His	His	Ile	Ser	His	Ser	705	710	715	720
5	Gly	Leu	Gly	Thr	Glu	Asn	Gly	His	Gly	Asn	Tyr	Asp	Val	Ile	Glu	Glu	725	730	735	
	Ile	Glu	Glu	Asn	Ser	His	Val	Asp	Ile	Lys	Ser	Glu	Leu	Gly	Tyr	Glu	740	745	750	
10	Gly	Gly	Gln	Asn	Ser	Gly	Asn	Gln	Ser	Phe	Glu	Glu	Asp	Thr	Glu	Glu	755	760	765	
	Asp	Lys	Pro	Lys	Tyr	Glu	Gln	Gly	Gly	Asn	Ile	Val	Asp	Ile	Asp	Phe	770	775	780	
15	Asp	Ser	Val	Pro	Gln	Ile	His	Gly	Gln	Asn	Lys	Gly	Asn	Gln	Ser	Phe	785	790	795	800
	Glu	Glu	Asp	Thr	Glu	Lys	Asp	Lys	Pro	Lys	Tyr	Glu	His	Gly	Gly	Asn	805	810	815	
20	Ile	Ile	Asp	Ile	Asp	Phe	Asp	Ser	Val	Pro	His	Ile	His	Gly	Phe	Asn	820	825	830	
	Lys	His	Thr	Glu	Ile	Ile	Glu	Glu	Asp	Thr	Asn	Lys	Asp	Lys	Pro	Ser	835	840	845	
25	Tyr	Gln	Phe	Gly	Gly	His	Asn	Ser	Val	Asp	Phe	Glu	Glu	Asp	Thr	Leu	850	855	860	
	Pro	Lys	Val	Ser	Gly	Gln	Asn	Glu	Gly	Gln	Gln	Thr	Ile	Glu	Glu	Asp	865	870	875	880
30	Thr	Thr	Pro	Pro	Ile	Val	Pro	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	885	890	895	
	Ser	Glu	Pro	Glu	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ser	Glu	900	905	910	
35	Pro	Glu	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ser	Glu	Pro	Glu	915	920	925	
40	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ala	Glu	Pro	Gly	Lys	Pro	930	935	940	
	Val	Pro	Pro	Ala	Lys	Glu	Glu	Pro	Lys	Lys	Pro	Ser	Lys	Pro	Val	Glu	945	950	955	960
45	Gln	Gly	Lys	Val	Val	Thr	Pro	Val	Ile	Glu	Ile	Asn	Glu	Lys	Val	Lys	965	970	975	
	Ala	Val	Ala	Pro	Thr	Lys	Lys	Pro	Gln	Ser	Lys	Lys	Ser	Glu	Leu	Pro	980	985	990	
50	Glu	Thr	Gly	Gly	Glu	Glu	Ser	Thr	Asn	Lys	Gly	Met	Leu	Phe	Gly	Gly	995	1000	1005	
55	Leu	Phe	Ser	Ile	Leu	Gly	Leu	Ala	Leu	Leu	Arg	Arg	Asn	Lys	Lys	Asn	1010	1015	1020	

His Lys Ala
1025

5 (2) INFORMATION FOR SEQ ID NO:5255:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 155 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5255:

20 Gly Glu Lys Cys Met Phe Leu Ala Trp Asn Glu Ile Arg Arg Asn Lys
 1 5 10 15
 Leu Lys Phe Gly Leu Ile Ile Gly Val Leu Thr Met Ile Ser Tyr Leu
 20 25 30
 Leu Phe Leu Leu Ser Gly Leu Ala Asn Gly Leu Ile Asn Met Asn Lys
 35 40 45
 Glu Gly Ile Asp Lys Trp Gln Ala Asp Ala Ile Val Leu Asn Lys Asp
 50 55 60
 Ala Asn Gln Thr Val Gln Gln Ser Val Phe Asn Lys Lys Asp Ile Glu
 65 70 75 80
 Asn Lys Tyr Lys Lys Gln Ala Thr Leu Lys Gln Thr Gly Glu Ile Val
 85 90 95
 Ser Asn Gly His Gln Lys Asp Asn Val Leu Val Phe Gly Val Glu Lys
 100 105 110
 Ser Ser Phe Leu Val Pro Ser Leu Ile Glu Gly His Lys Ala Thr Lys
 115 120 125
 Asp Asn Glu Val Leu Ala Asp Glu Thr Leu Lys Asn Lys Gly Leu Lys
 130 135 140
 Leu Gly Asp Thr Leu Ser Leu Ser Xaa Xaa Arg
 145 150 155

50 Claims

1. Computer readable medium having recorded thereon a nucleotide sequence of the Staphylococcus aureus genome as depicted in SEQ ID NOS:1-5,191, a representative fragment thereof or a nucleotide sequence at least 95 % identical to a nucleotide sequence depicted in SEQ ID NOS:1-5,191.
2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a degenerate variant thereof.

3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
- 5 4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
5. A computer-based system for identifying fragments of the *Staphylococcus aureus* genome of commercial importance comprising the following elements:
 - 10 (a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191;
 - (b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and
 - 15 (c) retrieval means for obtaining said homologous sequence(s) of step (b).
6. A method for identifying commercially important nucleic acid fragments of the *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.
- 20 7. A method for identifying an expression modulating fragment of *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.
- 25 8. A protein-encoding nucleic acid fragment of the *Staphylococcus aureus* genome, wherein said fragment comprises the nucleotide sequence of any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence, or a degenerate variant of any of the aforementioned sequences.
- 30 9. The nucleic acid fragment of claim 8 which is DNA.
10. The nucleic acid fragment of claim 8 which is RNA.
11. A vector comprising a fragment of claim 8.
- 40 12. A fragment of the *Staphylococcus aureus* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frames depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.
- 45 13. A vector comprising a fragment of claim 12.
14. A organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome of claim 8.
- 50 15. A method for producing a polypeptide in a host cell comprising the steps of:
 - (a) incubating an organism of claim 14 under conditions where said fragment is expressed to produce said protein, and
 - 55 (b) isolating said protein.
16. An organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome

of claim 12.

17. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 30 to 300 bases 5' to any one of the fragments of the *Staphylococcus aureus* genome depicted in Seq ID Nos:1-5,191 and Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.
18. A nucleic acid molecule being a homolog of any of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:
 - (a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS:1-5,191 and Tables 2 and 3, including fragments thereof;
 - (b) identifying members of said library which contain sequences that hybridize to said target sequence;
 - (c) isolating the nucleic acid molecules from said members identified in step (b).
19. A DNA molecule being a homolog of any one of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:
 - (a) isolating mRNA, DNA, or cDNA produced from an organism;
 - (b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Staphylococcus aureus* genome to prime said amplification;
 - (c) isolating said amplified sequences produced in step (b).
20. A polypeptide encoded by a fragment of claim 8.
21. An antibody which selectively binds to any one of the polypeptides of claim 20.
22. A kit for analyzing samples for the presence of polynucleotides derived from *Staphylococcus aureus*, comprising at least one polynucleotide containing a nucleotide sequence of any one of the fragments SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical thereto or a degenerate variant of any of the aforementioned sequences; that will hybridize to a *staphylococcus aureus* polynucleotide under stringent hybridization conditions, and a suitable container.
23. A *Staphylococcus aureus* polypeptide comprising an amino acid sequence identical to an amino acid sequence selected from the group consisting of SEQ ID NOS:5,192 to 5,255 or comprising an amino acid sequence having at least 95% identity to such a sequence.
24. A *Staphylococcus aureus* polypeptide antigen comprising at least one epitope derived from a *Staphylococcus aureus* polypeptide selected from the group consisting of SEQ ID NOS:5,192 to 5,255.
25. A polypeptide comprising at least one epitope encoded by a *Staphylococcus aureus* amino acid sequence selected from the group consisting of the epitopic sequences listed in Table 4.
26. The polypeptide of claim 24 or 26, wherein said polypeptide is fixed to a solid phase.
27. A diagnostic kit for detecting *Staphylococcus aureus* infection comprising
 - (a) an isolated polypeptide antigen of claim 24, and
 - (b) means for detecting the binding of an antibody contained in a biological fluid to said antigen.
28. A vaccine composition comprising a polypeptide of claim 24 present in a pharmaceutically acceptable carrier.
29. A method of vaccinating an individual against *Staphylococcus aureus* infection comprising, administering to an individual the vaccine composition of claim 28.

Figure 1

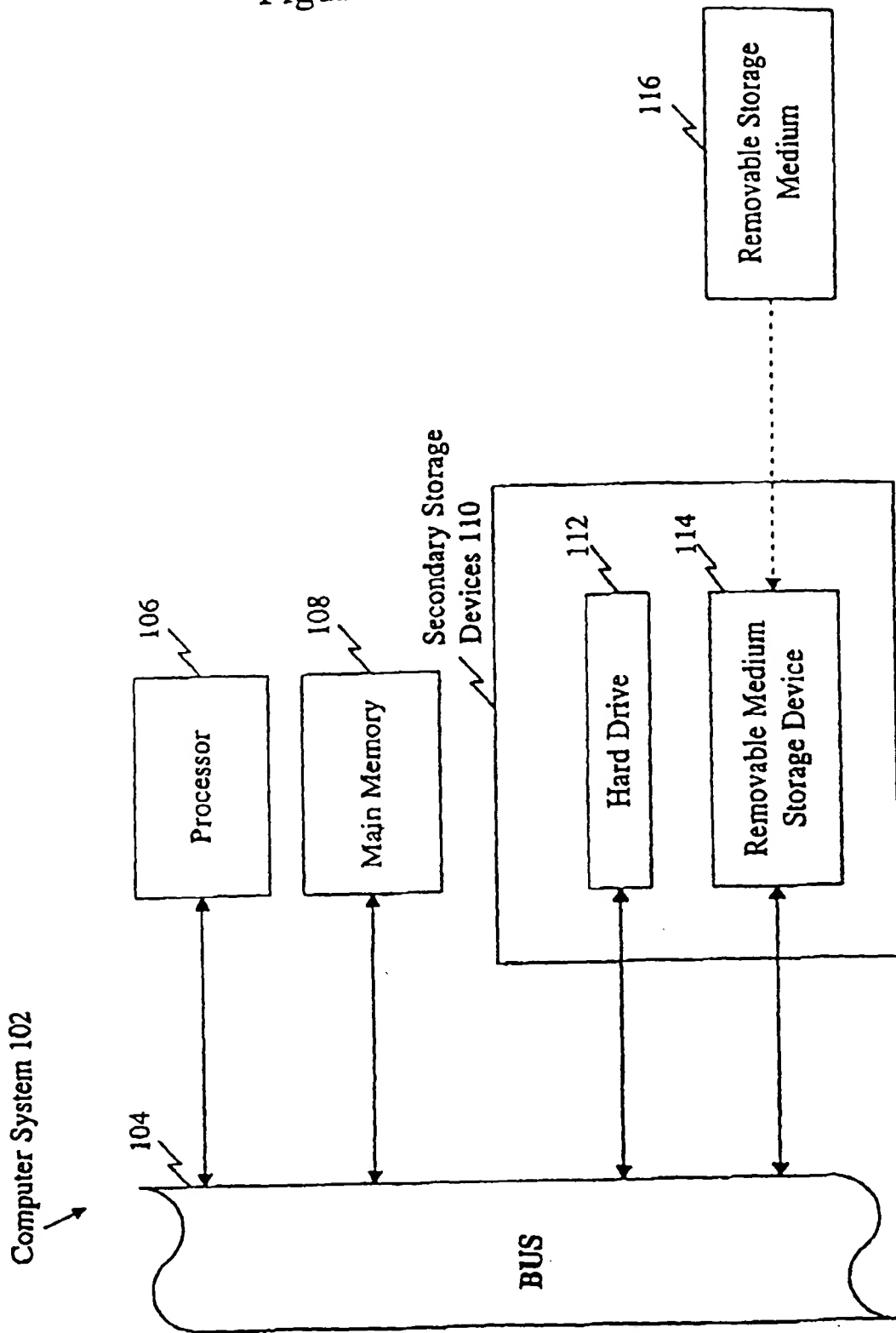
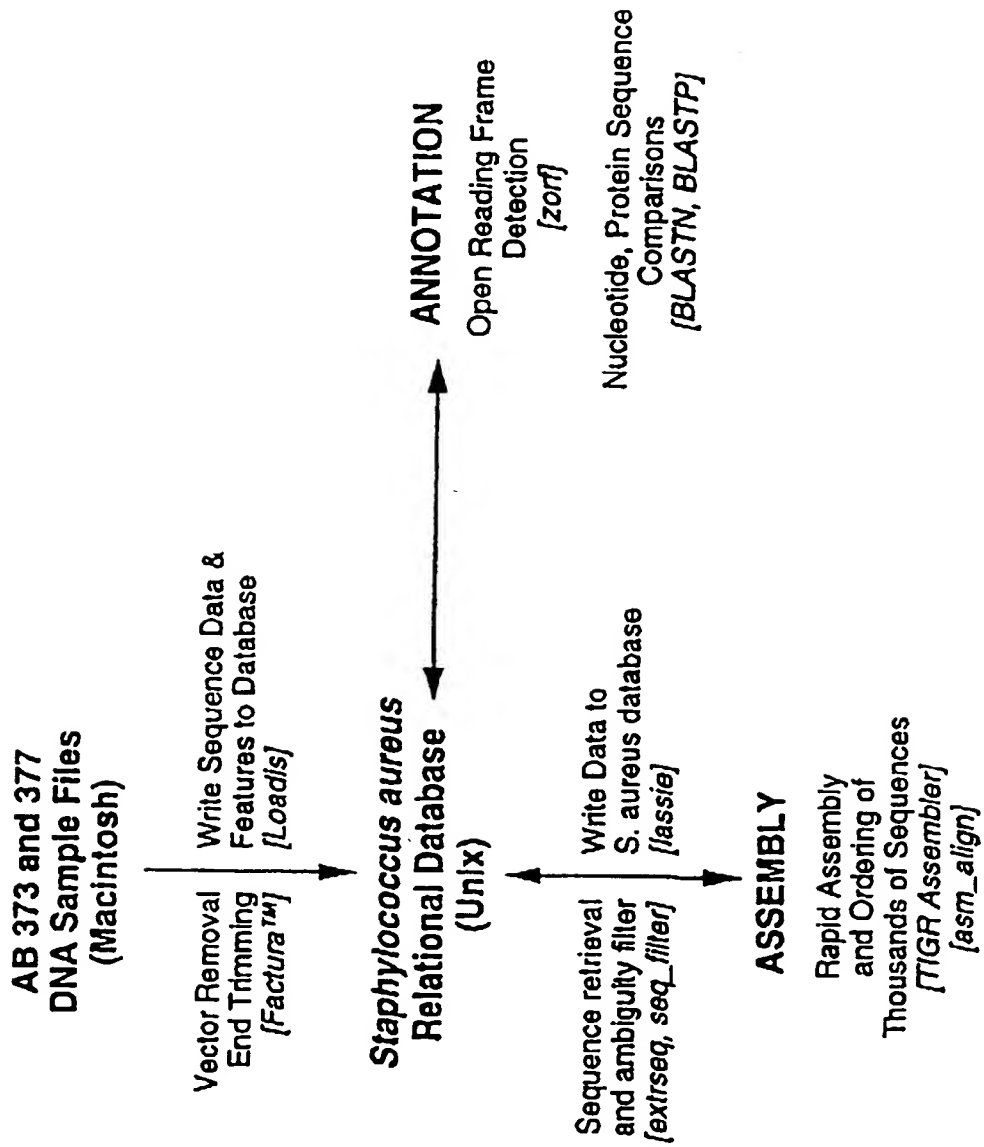
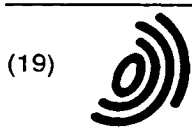


Figure 2





(19)

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(54) **Staphylococcus aureus polynucleotides and sequences**

(57) The present invention provides polynucleotide sequences of the genome of *Staphylococcus aureus*, polypeptide sequences encoded by the polynucleotide sequences, corresponding polynucleotides and polypeptides, vectors and hosts comprising the polynu-

cleotides, and assays and other uses thereof. The present invention further provides polynucleotide and polypeptide sequence information stored on computer readable media, and computer-based systems and methods which facilitate its use.

EP 0 786 519 A3



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which under Rule 45 of the European Patent Convention EP 97 10 0117
shall be considered, for the purposes of subsequent
proceedings, as the European search report

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INCOMPLETE SEARCH			
<p>The Search Division considers that the present application, or one or more of its claims, does/do not comply with the EPC to such an extent that a meaningful search into the state of the art cannot be carried out, or can only be carried out partially, for these claims.</p> <p>Claims searched completely :</p> <p>Claims searched incompletely :</p> <p>Claims not searched :</p> <p>Reason for the limitation of the search:</p> <p>Article 52 (2)(d) EPC - Presentation of information - Claims 1-4 concerns computer readable media characterised solely by the information stored thereon. However, search has been carried out as far as possible.</p>			
Place of search		Date of completion of the search	Examiner
MUNICH		31 July 1998	Chakravarty, A
<p>CATEGORY OF CITED DOCUMENTS</p> <p>X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document</p> <p>T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document</p>			

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